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<b>(54) Title:</b> HUMAN POTASSIUM CHANNEL GENES		
<b>(57) Abstract</b>		
<p>Methods for isolating <i>K+Hnov</i> genes are provided. The <i>K+Hnov</i> nucleic acid compositions find use in identifying homologous or related proteins and the DNA sequences encoding such proteins; in producing compositions that modulate the expression or function of the protein; and in studying associated physiological pathways. In addition, modulation of the gene activity <i>in vivo</i> is used for prophylactic and therapeutic purposes, such as identification of cell type based on expression, and the like.</p>		

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## HUMAN POTASSIUM CHANNEL GENES

### INTRODUCTION

#### *Background*

5 Ion channels are multi-subunit, membrane bound proteins critical for maintenance of cellular homeostasis in nearly all cell types. Channels are involved in a myriad of processes including modulation of action potentials, regulation of cardiac myocyte excitability, heart rate, vascular tone, neuronal signaling, activation and proliferation of T-cells, and insulin secretion from  
10 pancreatic islet cells. In humans, ion channels comprise extended gene families with hundreds, or perhaps thousands, of both closely related and highly divergent family members. The majority of known channels regulate the passage of sodium ( $\text{Na}^+$ ), chloride ( $\text{Cl}^-$ ), calcium ( $\text{Ca}^{++}$ ) and potassium ( $\text{K}^+$ ) ions across the cellular membrane.

15 Given their importance in maintaining normal cellular physiology, it is not surprising that ion channels have been shown to play a role in heritable human disease. Indeed, ion channel defects are involved in predisposition to epilepsy, cardiac arrhythmia (long QT syndrome), hypertension (Bartter's syndrome), cystic fibrosis, (defects in the CFTR chloride channel), several skeletal muscle disorders  
20 (hyperkalemic periodic paralysis, paramyotonia congenita, episodic ataxia) and congenital neural deafness (Jervell-Lange-Nielson syndrome), amongst others.

The potassium channel gene family is believed to be the largest and most diverse ion channel family.  $\text{K}^+$  channels have critical roles in multiple cell types and pathways, and are the focus of significant investigation. Four human  
25 conditions, episodic ataxia with myokymia, long QT syndrome, epilepsy and Bartter's syndrome have been shown to be caused by defective  $\text{K}^+$  ion channels. As the  $\text{K}^+$  channel family is very diverse, and given that these proteins are critical components of virtually all cells, it is likely that abnormal  $\text{K}^+$  channels will be involved in the etiology of additional renal, cardiovascular and central nervous  
30 system disorders of interest to the medical and pharmaceutical community.

The  $\text{K}^+$  channel superfamily can be broadly classified into groups, based upon the number of transmembrane domain (TMD) segments in the mature

protein. The minK (IsK) gene contains a single TMD, and although not a channel by itself, minK associates with different K<sup>+</sup> channel subunits, such as KvLQT1 and HERG to modify the activity of these channels. The inward rectifying K<sup>+</sup> channels (GIRK, IRK, CIR, ROMK) contain 2 TMD domains and a highly conserved pore domain. Twik-1 is a member of the newly emerging 4TMD K<sup>+</sup> channel subset. Twik-like channels (leak channels) are involved in maintaining the steady-state K<sup>+</sup> potentials across membranes and therefore the resting potential of the cell near the equilibrium potential for potassium (Duprat *et al.* (1997) EMBO J 16(17):5464-5471). These proteins are particularly intriguing targets for therapeutic regulation.

10 The 6TMD, or Shaker-like channels, presently comprise the largest subset of known K<sup>+</sup> channels. The slopoke (slo) related channels, or Ca<sup>2+</sup> regulated channels apparently have either 10 TMD, or 6 TMD with 4 additional hydrophobic domains.

Four transmembrane domain, tandem pore domain K<sup>+</sup> channels (4T/2P channels) represent a new family of potassium selective ion channels involved in the control of background membrane conductances. In mammals, five channels fitting the 4T/2P architecture have been described: TWIK, TREK, TASK-1, TASK-2 and TRAAK. The 4T/2P channels all have distinct characteristics, but are all thought to be involved in maintaining the steady-state K<sup>+</sup> potentials across membranes and therefore the resting potential of the cell near the equilibrium potential for potassium (Duprat *et al.* (1997) EMBO J 16(17):5464-5471). These proteins are particularly intriguing targets for therapeutic regulation. Within this group, TWIK-1, TREK-1 and TASK-1 and TASK-2 are widely distributed in many different tissues, while TRAAK is present exclusively in brain, spinal cord and retina. The 4T/2P channels have different physiologic properties; TREK-1 channels, are outwardly rectifying (Fink *et al.* (1996) EMBO J 15(24):6854-62), while TWIK-1 channels, are inwardly rectifying (Lesage *et al.* (1996) EMBO J 15(5):1004-11. TASK channels are regulated by changes in PH while TRAAK channels are stimulated by arachidonic acid (Reyes *et al.* (1998) JBC 273(47):30863-30869).

25 30

The degree of sequence homology between different K<sup>+</sup> channel genes is substantial. At the amino acid level, there is about 40% similarity between



different human genes, with distinct regions having higher homology, specifically the pore domain. It has been estimated that the K<sup>+</sup> channel gene family contains approximately 10<sup>2</sup>-10<sup>3</sup> individual genes. Despite the large number of potential genes, an analysis of public sequence databases and the scientific literature demonstrates that only a small number, approximately 20-30, have been identified. This analysis suggests that many of these important genes remain to be identified.

Potassium channels are involved in multiple different processes and are important regulators of homeostasis in nearly all cell types. Their relevance to basic cellular physiology and role in many human diseases suggests that pharmacological agents could be designed to specific channel subtypes and these compounds then applied to a large market (Bulman, D.E. (1997) Hum Mol Genet 6:1679-1685; Ackerman, M.J. and Clapham D.E. (1997) NEJM 336:1575-1586, Curran, M.E. (1998) Current Opinion in Biotechnology 9:565-572). The variety of therapeutic agents that modulate K<sup>+</sup> channel activity reflects the diversity of physiological roles and importance of K<sup>+</sup> channels in cellular function. A difficulty encountered in therapeutic use of therapeutic agents that modify K<sup>+</sup> channel activity is that the presently available compounds tend to be non-specific and elicit both positive and negative responses, thereby reducing clinical efficacy. To facilitate development of specific compounds it is desirable to have further characterize novel K<sup>+</sup> channels for use in *in vitro* and *in vivo* assays.

#### *Relevant Literature*

A large body of literature exists in the general area of potassium channels. A review of the literature may be found in the series of books, "The Ion Channel Factsbook", volumes 1-4, by Edward C. Conley and William J. Brammar, Academic Press. An overview is provided of: extracellular ligand-gated ion channels (ISBN: 0121844501), intracellular ligand-gated channels (ISBN: 012184451X), Inward rectifier and intercellular channels (ISBN: 0121844528), and voltage gated channels (ISBN: 0121844536). Hille, B. (1992) "Ionic Channels of Excitable Membranes", 2<sup>nd</sup> Ed. Sunderland MA: Sinauer Associates, also reviews potassium channels.

Jan and Jan (1997) Annu. Rev. Neurosci. 20:91-123 review cloned potassium channels from eukaryotes and prokaryotes. Ackerman and Clapham (1997) N. Engl. J. Med. 336:1575-1586 discuss the basic science of ion channels in connection with clinical disease. Bulman (1997) Hum. Mol. Genet. 6:1679-1685 describe some phenotypic variation in ion channel disorders.

Stephan *et al.* (1994) Neurology 44:1915-1920 describe a pedigree segregating a myotonia with muscular hypertrophy and hyperirritability as an autosomal dominant trait (rippling muscle disease, Ricker *et al.* (1989) Arch. Neurol. 46:405-408). Electromyography demonstrated that mechanical stimulation provoked electrically silent contractions. The responsible gene was localized to the distal end of the long arm of chromosome 1, in a 12-cM region near D1S235.

Type II pseudohypoaldosteronism is the designation used for a syndrome of chronic mineralocorticoid-resistant hyperkalemia with hypertension. The primary abnormality in type II PHA is thought to be a specific defect of the renal secretory mechanism for potassium, which limits the kaliuretic response to, but not the sodium and chloride reabsorptive effect of, mineralocorticoid. By analysis of linkage in families with autosomal dominant transmission, Mansfield *et al.* (1997) Nature Genet. 16:202-205 demonstrated locus heterogeneity of the trait, with linkage of the PHA2 gene to 1q31-q42 and 17p11-q21.

Sequences of four transmembrane, two pore potassium channels have been previously described. Reyes *et al.* (1998) J Biol Chem 273(47):30863-30869 discloses a pH sensitive channel. As with the related TASK-1 and TRAAK channels, the outward rectification is lost at high external K<sup>+</sup> concentration. The TRAAK channel is described by Fink *et al.* (1998) EMBO J 17(12):3297-308. A cardiac two-pore channel is described in Kim *et al.* (1998) Circ Res 82(4):513-8. An open rectifier potassium channel with two pore domains in tandem and having a postsynaptic density protein binding sequence at the C terminal was cloned by Leonoudakis *et al.* (1998) J Neurosci 18(3):868-77.

The electrophysiological properties of Task channels are of interest, (Duprat *et al.* (1997) EMBO J 16:5464-71). TASK currents are K<sup>+</sup>-selective, instantaneous and non-inactivating. They show an outward rectification when external [K<sup>+</sup>] is low, which is not observed for high [K<sup>+</sup>]<sub>out</sub>, suggesting a lack of

intrinsic voltage sensitivity. The absence of activation and inactivation kinetics as well as voltage independence are characteristic of conductances referred to as leak or background conductances. TASK is very sensitive to variations of extracellular pH in a narrow physiological range, a property probably essential for its physiological function, and suggests that small pH variations may serve a communication role in the nervous system.

#### SUMMARY OF THE INVENTION

Isolated nucleotide compositions and sequences are provided for *K+Hnov* genes. The *K+Hnov* nucleic acid compositions find use in identifying homologous or related genes; in producing compositions that modulate the expression or function of its encoded proteins; for gene therapy; mapping functional regions of the proteins; and in studying associated physiological pathways. In addition, modulation of the gene activity *in vivo* is used for prophylactic and therapeutic purposes, such as treatment of potassium channel defects, identification of cell type based on expression, and the like.

#### DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Nucleic acid compositions encoding *K+Hnov* polypeptides are provided. They are used in identifying homologous or related genes; in producing compositions that modulate the expression or function of the encoded proteins; for gene therapy; mapping functional regions of the proteins; and in studying associated physiological pathways. The *K+Hnov* gene products are members of the potassium channel gene family, and have high degrees of homology to known potassium channels. The encoded polypeptides may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity.

#### CHARACTERIZATION OF *K+HNOV*

The sequence data predict that the provided *K+Hnov* genes encode potassium channels. Table 1 summarizes the DNA sequences, corresponding SEQ ID NOs, chromosomal locations, and polymorphisms. The provided

sequences may encode a predicted K<sup>+</sup> channel, e.g. voltage gated, inward rectifier, etc.; or a modulatory subunit.

Electrophysiologic characterization of ion channels is an important part of understanding channel function. Full length ion channel cDNAs may be combined with proper vectors to form expression constructs of each individual channel. Functional analyses of expressed channels can be performed in heterologous systems, or by expression in mammalian cell lines. For expression analyses in heterologous systems such as *Xenopus* oocytes, synthetic mRNA is made through *in vitro* transcription of each channel construct. mRNA is then injected, singly or in combination with interacting channel subunit mRNAs, into prepared oocytes and the cells allowed to express the channel for several days. Oocytes expressing the channel of interest are then analyzed by whole cell voltage clamp and patch clamp techniques.

To determine the properties of each channel when expressed in mammalian cells expression vectors specific to this type of analyses may be constructed and the resultant construct used to transform the target cells (for example human embryonic kidney (HEK) cells). Both stable and transiently expressing lines may be studied using whole cell voltage clamp and patch clamp techniques. Data obtained from EP studies includes, but is not limited to: current profiles elicited by depolarization and hyperpolarization, current-voltage (I-V) relationships, voltage dependence of activation, biophysical kinetics of channel activation, deactivation, and inactivation, reversal potential, ion selectivity, gating properties and sensitivity to channel antagonists and agonists.

Heterologous or mammalian cell lines expressing the novel channels can be used to characterize small molecules and drugs which interact with the channel. The same experiments can be used to assay for novel compounds which interact with the expressed channels.

In many cases the functional ion channel formed by K<sup>+</sup> channel polypeptides will be heteromultimers. Heteromultimers are known to form between different voltage gated, outward rectifying potassium channel  $\alpha$  subunits, generally comprising four subunits, and frequently associated with auxiliary,  $\beta$  subunits. Typically such  $\alpha$  subunits share a six-transmembrane domain structure (S1-S6),

with one highly positively charged domain (S4) and a pore region situated between S5 and S6. Examples of such subunits are K+Hnov4, K+Hnov9, and K+Hnov12. Channels are also formed by multimerization of subunits of the two transmembrane and one pore architecture. It is predicted that two subunits of  
5 K+Hnov49 or K+Hnov59 will be required to form a functional channel.

Heteromultimers of greatest interest are those that form between subunits expressed in the same tissues, and are a combination of subunits from the same species. In addition, the formation of multimers between the subject polypeptides and subunits that form functional channels are of particular interest. The resulting  
10 channel may have decreased or increased conductance relative to a homomultimer, and may be altered in response to beta subunits or other modulatory molecules.

Known voltage gated K<sup>+</sup> channel  $\alpha$  subunits include Kv1.1-1.8 (Gutman *et al.* (1993) *Sem. Neurosci.* 5:101-106); Kv2.1-2.2; Kv3.1-3.4; Kv4.1-4.3; Kv5.1;  
15 Kv6.1; Kv7.1; Kv8.1; Kv9.1-9.2. The subunits capable of forming ion inducing channels include all of those in the Kv1 through Kv4; and Kv7 families. The Kv5.1, Kv6.1, Kv8.1 and Kv9.1-9.2 subunits may be electrically silent, but functional in modifying the properties in heteromultimers.

TABLE 1

Name	cDNA SEQ	Protein SEQ	Polymorphisms	Chromosome Position	Channel Type
K+Hnov1	SEQ ID NO:1	SEQ ID NO:2	Alternative poly(A) tail: 1236, 2395	2q37	ATP-sensitive inward rectifying
K+Hnov4	SEQ ID NO:3	SEQ ID NO:4	A312C T335C A377G T344C A401G CA410-411GG (Ala/Thr)	unknown	Voltage gated K+ channel
K+Hnov6	SEQ ID NO:5	SEQ ID NO:6		2p23	Delayed rectifying K+ channel
K+Hnov9	SEQ ID NO:7	SEQ ID NO:8	Alternative poly(A) tail: 2304	8q23	Voltage gated K+ channel
K+Hnov12	SEQ ID NO:9	SEQ ID NO:10	C321T (Pro/Leu) A375G (Glu/Gly) C407T (Leu/Phe)	Xp21	Voltage gated K+ channel
K+Hnov15	SEQ ID NO:11	SEQ ID NO:12	Alternative poly(A) tail: 1427 A689G (Gly/Arg)	13q14	modulatory subunit
K+Hnov27	SEQ ID NO:13	SEQ ID NO:14	T365A (Ile/Asn)	18q12	modulatory subunit
K+Hnov2	SEQ ID NO:15	SEQ ID NO:16	N/A	N/A	4 transmembrane domain, 2 pore domain K+ channel

K+Hnov 11	SEQ ID NO:17	SEQ ID NO:18	N/A	N/A	Human ortholog of murine gene, 6 transmembrane domains, voltage gated, delayed rectifier K <sup>+</sup> channel
K+Hnov 14	SEQ ID NO:19	SEQ ID NO:20	C3168T	12q14	6 transmembrane domain, voltage gated K <sup>+</sup> channel
K+Hnov28	SEQ ID NO:21-24	SEQ ID NO:25	4 alternative 5' splices	3q29	Modulatory subunit
K+Hnov42	SEQ ID NO:26	SEQ ID NO:27	G1162A; T1460A; T2496A	8q11	Homology to K <sup>+</sup> channel protein of <i>C. elegans</i>
K+Hnov44	SEQ ID NO:28-29	SEQ ID NO:30	N/A	22p13	beta-subunit
K+Hnov49	SEQ ID NO:80	SEQ ID NO:81	(ATCT) <sub>n</sub> repeats in the 3' UTR sequence, starting at position 2186	1q41	4T2P - channel; linked to the disease loci for rippling muscle disease 1 (RMD1), and type II pseudohypoparathyroidism
K+Hnov59	SEQ ID NO:82	SEQ ID NO:83	N/A	chr19	4T2P channel

### K+HNOV NUCLEIC ACID COMPOSITIONS

As used herein, the term "K+Hnov" is generically used to refer to any one of the provided genetic sequences listed in Table 1. Where a specific K+Hnov sequence is intended, the numerical designation, e.g. K49 or K59, will be added.

5 Nucleic acids encoding *K+Hnov* potassium channels may be cDNA or genomic DNA or a fragment thereof. The term "*K+Hnov* gene" shall be intended to mean the open reading frame encoding any of the provided *K+Hnov* polypeptides, introns, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but  
10 possibly further in either direction. The gene may be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome.

The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA  
15 species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, removed by nuclear RNA splicing, to create a continuous open reading frame encoding a K+Hnov protein.

A genomic sequence of interest comprises the nucleic acid present  
20 between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It may further include the 3' and 5' untranslated regions found in the mature mRNA. It may further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb,  
25 but possibly more, of flanking genomic DNA at either the 5' or 3' end of the transcribed region. The genomic DNA may be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' or 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for  
30 proper tissue and stage specific expression.



The sequence of the 5' flanking region may be utilized for promoter elements, including enhancer binding sites, that provide for developmental regulation in tissues where *K+Hnov* genes are expressed. The tissue specific expression is useful for determining the pattern of expression, and for providing  
5 promoters that mimic the native pattern of expression. Naturally occurring polymorphisms in the promoter regions are useful for determining natural variations in expression, particularly those that may be associated with disease.

Alternatively, mutations may be introduced into the promoter regions to determine the effect of altering expression in experimentally defined systems.  
10 Methods for the identification of specific DNA motifs involved in the binding of transcriptional factors are known in the art, e.g. sequence similarity to known binding motifs, gel retardation studies, etc. For examples, see Blackwell *et al.* (1995) Mol Med 1: 194-205; Mortlock *et al.* (1996) Genome Res. 6: 327-33; and Joulin and Richard-Foy (1995) Eur J Biochem 232: 620-626.

15 The regulatory sequences may be used to identify *cis* acting sequences required for transcriptional or translational regulation of *K+Hnov* expression, especially in different tissues or stages of development, and to identify *cis* acting sequences and *trans* acting factors that regulate or mediate *K+Hnov* expression. Such transcription or translational control regions may be operably linked to a  
20 *K+Hnov* gene in order to promote expression of wild type or altered *K+Hnov* or other proteins of interest in cultured cells, or in embryonic, fetal or adult tissues, and for gene therapy.

The nucleic acid compositions of the subject invention may encode all or a part of the subject polypeptides. Double or single stranded fragments may be  
25 obtained of the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, etc. For the most part, DNA fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and may be at least about 50 nt. Such small DNA fragments are useful as primers for PCR, hybridization screening probes, etc.  
30 Larger DNA fragments, i.e. greater than 100 nt are useful for production of the encoded polypeptide. For use in amplification reactions, such as PCR, a pair of

primers will be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers will hybridize to the subject sequence under stringent conditions, as known in the art. It is preferable to choose a pair of primers that will generate an amplification product of at least about 50 nt, preferably at least about 100 nt. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. Amplification primers hybridize to complementary strands of DNA, and will prime towards each other.

The *K+Hnov* genes are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the DNA will be obtained substantially free of other nucleic acid sequences that do not include a *K+Hnov* sequence or fragment thereof, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", i.e. flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The DNA may also be used to identify expression of the gene in a biological specimen. The manner in which one probes cells for the presence of particular nucleotide sequences, as genomic DNA or RNA, is well established in the literature and does not require elaboration here. DNA or mRNA is isolated from a cell sample. The mRNA may be amplified by RT-PCR, using reverse transcriptase to form a complementary DNA strand, followed by polymerase chain reaction amplification using primers specific for the subject DNA sequences. Alternatively, the mRNA sample is separated by gel electrophoresis, transferred to a suitable support, e.g. nitrocellulose, nylon, etc., and then probed with a fragment of the subject DNA as a probe. Other techniques, such as oligonucleotide ligation assays, *in situ* hybridizations, and hybridization to DNA probes arrayed on a solid chip may also find use. Detection of mRNA hybridizing to the subject sequence is indicative of *K+Hnov* gene expression in the sample.

The sequence of a *K+Hnov* gene, including flanking promoter regions and coding regions, may be mutated in various ways known in the art to generate targeted changes in promoter strength, sequence of the encoded protein, etc.

The DNA sequence or protein product of such a mutation will usually be substantially similar to the sequences provided herein, i.e. will differ by at least one nucleotide or amino acid, respectively, and may differ by at least two but not more than about ten nucleotides or amino acids. The sequence changes may be substitutions, insertions or deletions. Deletions may further include larger changes, such as deletions of a domain or exon. Other modifications of interest include epitope tagging, e.g. with the FLAG system, HA, etc. For studies of subcellular localization, fusion proteins with green fluorescent proteins (GFP) may be used.

Techniques for *in vitro* mutagenesis of cloned genes are known. Examples of protocols for site specific mutagenesis may be found in Gustin *et al.*, *Biotechniques* 14:22 (1993); Barany, *Gene* 37:111-23 (1985); Colicelli *et al.*, *Mol Gen Genet*, 199:537-9 (1985); and Prentki *et al.*, *Gene* 29:303-13 (1984). Methods for site specific mutagenesis can be found in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, CSH Press 1989, pp. 15.3-15.108; Weiner *et al.*, *Gene* 126:35-41 (1993); Sayers *et al.*, *Biotechniques* 13:592-6 (1992); Jones and Winistorfer, *Biotechniques* 12:528-30 (1992); Barton *et al.*, *Nucleic Acids Res* 18:7349-55 (1990); Marotti and Tomich, *Gene Anal Tech* 6:67-70 (1989); and Zhu, *Anal Biochem* 177:120-4 (1989). Such mutated genes may be used to study structure-function relationships of K+Hnov, or to alter properties of the protein that affect its function or regulation.

Homologs and orthologs of K+Hnov genes are identified by any of a number of methods. A fragment of the provided cDNA may be used as a hybridization probe against a cDNA library from the target organism of interest, where low stringency conditions are used. The probe may be a large fragment, or one or more short degenerate primers. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 6XSSC (0.9 M sodium chloride/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC (0.15 M sodium chloride/0.015 M sodium citrate). Sequence identity may be determined by hybridization under stringent conditions, for example, at 50°C or higher and

0.1XSSC (15 mM sodium chloride/0.15 mM sodium citrate). Nucleic acids having a region of substantial identity to the provided K+Hnov sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided K+Hnov sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes may be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice, canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Between mammalian species, *e.g.* human and mouse, homologs have substantial sequence similarity, *i.e.* at least 75% sequence identity between nucleotide sequences, in some cases 80 or 90% sequence identity, and may be as high as 95% sequence identity between closely related species. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.*

A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al. (1990), J. Mol. Biol. 215:403-10. In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and may be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). Exemplary search parameters for use with the MPSRCH program in order to identify sequences of a desired sequence identity are as follows: gap open penalty: 12; and gap extension penalty: 1.

#### K+HNOV POLYPEPTIDES

The subject nucleic acid sequences may be employed for producing all or portions of K+Hnov polypeptides. For expression, an expression cassette may be employed. The expression vector will provide a transcriptional and translational initiation region, which may be inducible or constitutive, where the coding region

is operably linked under the transcriptional control of the transcriptional initiation region; and a transcriptional and translational termination region. These control regions may be native to a *K+Hnov* gene, or may be derived from exogenous sources.

5       The peptide may be expressed in prokaryotes or eukaryotes in accordance with conventional ways, depending upon the purpose for expression. For large scale production of the protein, a unicellular organism, such as *E. coli*, *B. subtilis*, *S. cerevisiae*, insect cells in combination with baculovirus vectors, or cells of a higher organism such as vertebrates, particularly mammals, e.g. COS 7 cells, 10 may be used as the expression host cells. In some situations, it is desirable to express the *K+Hnov* gene in eukaryotic cells, where the *K+Hnov* protein will benefit from native folding and post-translational modifications. Small peptides can also be synthesized in the laboratory. Peptides that are subsets of the complete *K+Hnov* sequence may be used to identify and investigate parts of the 15 protein important for function, or to raise antibodies directed against these regions.

Fragments of interest include the transmembrane and pore domains, the signal sequences, regions of interaction between subunits, etc. Such domains will usually include at least about 20 amino acids of the provided sequence, more 20 usually at least about 50 amino acids, and may include 100 amino acids or more, up to the complete domain. Binding contacts may be comprised of non-contiguous sequences, which are brought into proximity by the tertiary structure of the protein. The sequence of such fragments may be modified through manipulation of the coding sequence, as described above. Truncations may be 25 performed at the carboxy or amino terminus of the fragment, e.g. to determine the minimum sequence required for biological activity.

With the availability of the protein or fragments thereof in large amounts, by employing an expression host, the protein may be isolated and purified in accordance with conventional ways. A lysate may be prepared of the expression 30 host and the lysate purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, or other purification technique. The

purified protein will generally be at least about 80% pure, preferably at least about 90% pure, and may be up to and including 100% pure. Pure is intended to mean free of other proteins, as well as cellular debris.

The expressed K+Hnov polypeptides are useful for the production of antibodies, where short fragments provide for antibodies specific for the particular polypeptide, and larger fragments or the entire protein allow for the production of antibodies over the surface of the polypeptide. Antibodies may be raised to the wild-type or variant forms of K+Hnov. Antibodies may be raised to isolated peptides corresponding to specific domains, e.g. the pore domain and the transmembrane domain, or to the native protein.

Antibodies are prepared in accordance with conventional ways, where the expressed polypeptide or protein is used as an immunogen, by itself or conjugated to known immunogenic carriers, e.g. KLH, pre-S HBsAg, other viral or eukaryotic proteins, or the like. Various adjuvants may be employed, with a series of injections, as appropriate. For monoclonal antibodies, after one or more booster injections, the spleen is isolated, the lymphocytes immortalized by cell fusion, and then screened for high affinity antibody binding. The immortalized cells, i.e. hybridomas, producing the desired antibodies may then be expanded. For further description, see Monoclonal Antibodies: A Laboratory Manual, Harlow and Lane eds., Cold Spring Harbor Laboratories, Cold Spring Harbor, New York, 1988. If desired, the mRNA encoding the heavy and light chains may be isolated and mutagenized by cloning in *E. coli*, and the heavy and light chains mixed to further enhance the affinity of the antibody. Alternatives to *in vivo* immunization as a method of raising antibodies include binding to phage "display" libraries, usually in conjunction with *in vitro* affinity maturation.

#### K+HNOV GENOTYPING

The subject nucleic acid and/or polypeptide compositions may be used to genotyping and other analysis for the presence of polymorphisms in the sequence, or variation in the expression of the subject genes. Genotyping may be performed to determine whether a particular polymorphisms is associated with

a disease state or genetic predisposition to a disease state, particularly diseases associated with defects in excitatory properties of cells, e.g. cardiac, muscle, renal and neural cells. Disease of interest include rippling muscle disease, and type II psuedohypoaldosteronism.

5 Clinical disorders associated with K<sup>+</sup> channel defects include long-QT syndrome; a congenital disorder affecting 1 in 10,000-15,000. Affected individuals have a prolonged QT interval in the electrocardiogram due to a delayed repolarization of the ventricle. Genetic linkage analyses identified two loci for long QT syndrome, LQT1, in 11p15.5 and LQT2, in 7q35-36. Positional  
10 cloning techniques identified the novel K<sup>+</sup> channel KvLQT1 on chromosome 11 while candidate gene analysis identified causative mutations in the HERG K<sup>+</sup> channel for LQT2.

The weaver mouse exhibits several abnormal neurological symptoms, including severe ataxia, loss of granule cell neurons in the cerebellum and  
15 dopaminergic cells in the substantia nigra, as well as seizures and male infertility. A G-protein-coupled K<sup>+</sup> channel having a mutation in the conserved pore domain has been determined to cause the disease. The pancreatic-islet  $\beta$ -cell ATP-sensitive K<sup>+</sup> channel (KATP) is composed of two subunits, the sulfonylurea receptor (SUR) and the inward rectifier K<sup>+</sup> channel Kir6.2. Mutations in both SUR  
20 and Kir6.2 have been identified in patients with persistent hyperinsulinemic hypoglycemia of infancy, which is caused by unregulated secretion of insulin.

Genotyping may also be performed for pharmacogenetic analysis to assess the association between an individual's genotype and that individual's ability to react to a therapeutic agent. Differences in target sensitivity can lead to  
25 toxicity or therapeutic failure. Relationships between polymorphisms in channel expression or specificity can be used to optimize therapeutic dose administration.

Genetic polymorphisms are identified in the K<sup>+</sup>Hnov gene (examples are listed in table 1), e.g. the repeat variation in the 3' UTR of K49. Nucleic acids comprising the polymorphic sequences are used to screen patients for altered  
30 reactivity and adverse side effects in response to drugs that act on K<sup>+</sup> channels.

K+Hnov genotyping is performed by DNA or RNA sequence and/or hybridization analysis of any convenient sample from a patient, e.g. biopsy material, blood sample, scrapings from cheek, etc. A nucleic acid sample from an individual is analyzed for the presence of polymorphisms in K+Hnov, particularly those that affect the activity, responsiveness or expression of K+Hnov. Specific sequences of interest include any polymorphism that leads to changes in basal expression in one or more tissues, to changes in the modulation of K+Hnov expression, or alterations in K+Hnov specificity and/or activity.

The effect of a polymorphism in K+Hnov gene sequence on the response to a particular agent may be determined by *in vitro* or *in vivo* assays. Such assays may include monitoring during clinical trials, testing on genetically defined cell lines, etc. The response of an individual to the agent can then be predicted by determining the K+Hnov genotype with respect to the polymorphism. Where there is a differential distribution of a polymorphism by racial background, guidelines for drug administration can be generally tailored to a particular ethnic group.

Biochemical studies may be performed to determine whether a sequence polymorphism in a *K+Hnov* coding region or control regions is associated with disease, for example the association of K+Hnov 9 with idiopathic generalized epilepsy. Disease associated polymorphisms may include deletion or truncation of the gene, mutations that alter expression level, that affect the electrical activity of the channel, etc.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. The nucleic acid may be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis. The use of the polymerase chain reaction is described in Saiki *et al.* (1985) *Science* 239:487, and a review of current techniques may be found in Sambrook *et al.* *Molecular Cloning: A Laboratory Manual*, CSH Press 1989, pp.14.2-14.33. Amplification may be used



to determine whether a polymorphism is present, by using a primer that is specific for the polymorphism. Alternatively, various methods are known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, for examples see Riley *et al.* (1990) N.A.R. 18:2887-2890; and Delahunty *et al.* 5 (1996) Am. J. Hum. Genet. 58:1239-1246.

A detectable label may be included in an amplification reaction. Suitable labels include fluorochromes, e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine 10 (ROX), 6-carboxy-2',4',7',4,7'-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, e.g. <sup>32</sup>P, <sup>35</sup>S, <sup>3</sup>H; etc. The label may be a two-stage system, where the amplified DNA is conjugated to biotin, haptens, etc. having a high affinity binding partner, e.g. avidin, specific antibodies, etc., where the binding partner is 15 conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

The sample nucleic acid, e.g. amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid may be 20 sequenced by dideoxy or other methods. Hybridization with the variant sequence may also be used to determine its presence, by Southern blots, dot blots, etc. The hybridization pattern of a control and variant sequence to an array of oligonucleotide probes immobilised on a solid support, as described in U.S. 5,445,934, or in WO95/35505, may also be used as a means of detecting the 25 presence of variant sequences. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), mismatch cleavage detection, and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys 30 a recognition site for a restriction endonuclease (restriction fragment length polymorphism, RFLP), the sample is digested with that endonuclease, and the

products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

In one embodiment of the invention, an array of oligonucleotides are provided, where discrete positions on the array are complementary to one or more of the provided sequences, e.g. oligonucleotides of at least 12 nt, frequently 20 nt, or larger, and including the sequence flanking a polymorphic position in a K<sup>+</sup>Hnov sequence; coding sequences for different K<sup>+</sup>Hnov channels, panels of ion channels comprising one or more of the provided K<sup>+</sup> channels; *etc.* Such an array may comprise a series of oligonucleotides, each of which can specifically hybridize to a different polymorphism. For examples of arrays, see Hacia *et al.* (1996) Nature Genetics 14:441-447; Lockhart *et al.* (1996) Nature Biotechnol. 14:1675-1680; and De Risi *et al.* (1996) Nature Genetics 14:457-460.

Screening for polymorphisms in K<sup>+</sup>Hnov may be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that may affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in K<sup>+</sup>Hnov proteins may be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded K<sup>+</sup>Hnov protein as a potassium channel may be determined by comparison with the wild-type protein.

Antibodies specific for a K<sup>+</sup>Hnov may be used in staining or in immunoassays. Samples, as used herein, include biological fluids such as semen, blood, cerebrospinal fluid, tears, saliva, lymph, dialysis fluid and the like; organ or tissue culture derived fluids; and fluids extracted from physiological tissues. Also included in the term are derivatives and fractions of such fluids. The cells may be dissociated, in the case of solid tissues, or tissue sections may be analyzed. Alternatively a lysate of the cells may be prepared.

Diagnosis may be performed by a number of methods to determine the absence or presence or altered amounts of normal or abnormal K<sup>+</sup>Hnov polypeptides in patient cells. For example, detection may utilize staining of cells

or histological sections, performed in accordance with conventional methods. The antibodies of interest are added to the cell sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody may be labeled with radioisotopes, enzymes, fluorescers, chemiluminescers, or other labels for direct detection. Alternatively, a second stage antibody or reagent is used to amplify the signal. Such reagents are well known in the art. For example, the primary antibody may be conjugated to biotin, with horseradish peroxidase-conjugated avidin added as a second stage reagent. Alternatively, the secondary antibody conjugated to a fluorescent compound, e.g. fluorescein, rhodamine, Texas red, etc. Final detection uses a substrate that undergoes a color change in the presence of the peroxidase. The absence or presence of antibody binding may be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, etc.

15

#### MODULATION OF GENE EXPRESSION

The K+Hnov genes, gene fragments, or the encoded protein or protein fragments are useful in gene therapy to treat disorders associated with K+Hnov defects. Expression vectors may be used to introduce the K+Hnov gene into a cell. Such vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences. Transcription cassettes may be prepared comprising a transcription initiation region, the target gene or fragment thereof, and a transcriptional termination region. The transcription cassettes may be introduced into a variety of vectors, e.g. plasmid; retrovirus, e.g. lentivirus; adenovirus; and the like, where the vectors are able to transiently or stably be maintained in the cells, usually for a period of at least about one day, more usually for a period of at least about several days to several weeks.

The gene or K+Hnov protein may be introduced into tissues or host cells by any number of routes, including viral infection, microinjection, or fusion of vesicles. Jet injection may also be used for intramuscular administration, as

described by Furth *et al.* (1992) Anal Biochem 205:365-368. The DNA may be coated onto gold microparticles, and delivered intradermally by a particle bombardment device, or "gene gun" as described in the literature (see, for example, Tang *et al.* (1992) Nature 356:152-154), where gold microprojectiles are coated with the K+Hnov or DNA, then bombarded into skin cells.

Antisense molecules can be used to down-regulate expression of K+Hnov in cells. The anti-sense reagent may be antisense oligonucleotides (ODN), particularly synthetic ODN having chemical modifications from native nucleic acids, or nucleic acid constructs that express such anti-sense molecules as RNA.

The antisense sequence is complementary to the mRNA of the targeted gene, and inhibits expression of the targeted gene products. Antisense molecules inhibit gene expression through various mechanisms, e.g. by reducing the amount of mRNA available for translation, through activation of RNase H, or steric hindrance. One or a combination of antisense molecules may be administered, where a combination may comprise multiple different sequences.

Antisense molecules may be produced by expression of all or a part of the target gene sequence in an appropriate vector, where the transcriptional initiation is oriented such that an antisense strand is produced as an RNA molecule. Alternatively, the antisense molecule is a synthetic oligonucleotide. Antisense oligonucleotides will generally be at least about 7, usually at least about 12, more usually at least about 20 nucleotides in length, and not more than about 500, usually not more than about 50, more usually not more than about 35 nucleotides in length, where the length is governed by efficiency of inhibition, specificity, including absence of cross-reactivity, and the like. It has been found that short oligonucleotides, of from 7 to 8 bases in length, can be strong and selective inhibitors of gene expression (see Wagner *et al.* (1996) Nature Biotechnology 14:840-844).

A specific region or regions of the endogenous sense strand mRNA sequence is chosen to be complemented by the antisense sequence. Selection of a specific sequence for the oligonucleotide may use an empirical method, where several candidate sequences are assayed for inhibition of expression of

the target gene in an *in vitro* or animal model. A combination of sequences may also be used, where several regions of the mRNA sequence are selected for antisense complementation.

Antisense oligonucleotides may be chemically synthesized by methods known in the art (see Wagner *et al.* (1993) *supra.* and Milligan *et al.*, *supra.*) Preferred oligonucleotides are chemically modified from the native phosphodiester structure, in order to increase their intracellular stability and binding affinity. A number of such modifications have been described in the literature, which alter the chemistry of the backbone, sugars or heterocyclic bases.

Among useful changes in the backbone chemistry are phosphorothioates; phosphorodithioates, where both of the non-bridging oxygens are substituted with sulfur; phosphoroamidites; alkyl phosphotriesters and boranophosphates. Achiral phosphate derivatives include 3'-O'-5'-S-phosphorothioate, 3'-S-5'-O-phosphorothioate, 3'-CH<sub>2</sub>-5'-O-phosphonate and 3'-NH-5'-O-phosphoroamidate. Peptide nucleic acids replace the entire ribose phosphodiester backbone with a peptide linkage. Sugar modifications are also used to enhance stability and affinity. The  $\alpha$ -anomer of deoxyribose may be used, where the base is inverted with respect to the natural  $\beta$ -anomer. The 2'-OH of the ribose sugar may be altered to form 2'-O-methyl or 2'-O-allyl sugars, which provides resistance to degradation without comprising affinity. Modification of the heterocyclic bases must maintain proper base pairing. Some useful substitutions include deoxyuridine for deoxythymidine; 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. 5-propynyl-2'-deoxyuridine and 5-propynyl-2'-deoxycytidine have been shown to increase affinity and biological activity when substituted for deoxythymidine and deoxycytidine, respectively.

As an alternative to anti-sense inhibitors, catalytic nucleic acid compounds, e.g. ribozymes, anti-sense conjugates, *etc.* may be used to inhibit gene expression. Ribozymes may be synthesized *in vitro* and administered to the patient, or may be encoded on an expression vector, from which the ribozyme is synthesized in the targeted cell (for example, see International patent application

WO 9523225, and Beigelman et al. (1995) Nucl. Acids Res 23:4434-42). Examples of oligonucleotides with catalytic activity are described in WO 9506764. Conjugates of anti-sense ODN with a metal complex, e.g. terpyridylCu(II), capable of mediating mRNA hydrolysis are described in Bashkin et al. (1995) Appl Biochem Biotechnol 54:43-56.

#### GENETICALLY ALTERED CELL OR ANIMAL MODELS FOR K+HNOV FUNCTION

The subject nucleic acids can be used to generate transgenic animals or site specific gene modifications in cell lines. Transgenic animals may be made through homologous recombination, where the normal *K+Hnov* locus is altered. Alternatively, a nucleic acid construct is randomly integrated into the genome. Vectors for stable integration include plasmids, retroviruses and other animal viruses, YACs, and the like.

The modified cells or animals are useful in the study of *K+Hnov* function and regulation. For example, a series of small deletions and/or substitutions may be made in the *K+Hnov* gene to determine the role of different transmembrane domains in forming multimeric structures, ion channels, etc. Of interest are the use of *K+Hnov* to construct transgenic animal models for epilepsy and other neurological defects, where expression of K+Hnov is specifically reduced or absent. Specific constructs of interest include anti-sense *K+Hnov*, which will block K+Hnov expression, expression of dominant negative K+Hnov mutations, etc. One may also provide for expression of the *K+Hnov* gene or variants thereof in cells or tissues where it is not normally expressed or at abnormal times of development.

DNA constructs for homologous recombination will comprise at least a portion of the *K+Hnov* gene with the desired genetic modification, and will include regions of homology to the target locus. DNA constructs for random integration need not include regions of homology to mediate recombination. Conveniently, markers for positive and negative selection are included. Methods for generating cells having targeted gene modifications through homologous recombination are

known in the art. For various techniques for transfecting mammalian cells, see Keown *et al.* (1990) Methods in Enzymology **185**:527-537.

For embryonic stem (ES) cells, an ES cell line may be employed, or embryonic cells may be obtained freshly from a host, e.g. mouse, rat, guinea pig, etc. Such cells are grown on an appropriate fibroblast-feeder layer or grown in the presence of leukemia inhibiting factor (LIF). When ES or embryonic cells have been transformed, they may be used to produce transgenic animals. After transformation, the cells are plated onto a feeder layer in an appropriate medium. Cells containing the construct may be detected by employing a selective medium. After sufficient time for colonies to grow, they are picked and analyzed for the occurrence of homologous recombination or integration of the construct. Those colonies that are positive may then be used for embryo manipulation and blastocyst injection. Blastocysts are obtained from 4 to 6 week old superovulated females. The ES cells are trypsinized, and the modified cells are injected into the blastocoel of the blastocyst. After injection, the blastocysts are returned to each uterine horn of pseudopregnant females. Females are then allowed to go to term and the resulting offspring screened for the construct. By providing for a different phenotype of the blastocyst and the genetically modified cells, chimeric progeny can be readily detected.

The chimeric animals are screened for the presence of the modified gene and males and females having the modification are mated to produce homozygous progeny. If the gene alterations cause lethality at some point in development, tissues or organs can be maintained as allogeneic or congenic grafts or transplants, or in *in vitro* culture. The transgenic animals may be any non-human mammal, such as laboratory animals, domestic animals, etc. The transgenic animals may be used in functional studies, drug screening, etc., e.g. to determine the effect of a candidate drug on Ras or related gene activation, oncogenesis, etc.

TESTING OF K<sup>+</sup>HNOV FUNCTION and RESPONSES

Potassium channels such as K<sup>+</sup>Hnov polypeptides are involved in multiple biologically important processes. Pharmacological agents designed to affect only specific channel subtypes are of particular interest. Presently available  
5 compounds tend to be non-specific and elicit both positive and negative responses, thereby reducing clinical efficacy.

The subject polypeptides may be used in *in vitro* and *in vivo* models to test the specificity of novel compounds, and of analogs and derivatives of compounds known to act on potassium channels. Numerous pharmacological agents have  
10 profound effects on K<sup>+</sup> channel activity. As examples, Sotalol (BETAPACE) is a class III antiarrhythmic drug that prolongs cardiac action potentials by inhibiting delayed rectifier K<sup>+</sup> channels. Sulfonylurea drugs, such as Glipizide (GLUCOTROL) and Tolazamide (TOLAMIDE) function as antidiabetic drugs by blocking ATP-sensitive K<sup>+</sup> channels present in pancreatic islet cells, thereby  
15 regulating insulin secretion. Diazoxide (HYPERSTAT IV) is an antihypertensive drug that activates ATP-sensitive K<sup>+</sup> channels, resulting in the relaxation of vascular smooth muscle. There are several other examples of drugs that have antidiabetic, antihypertensive, or antiarrhythmic activities. A number of drugs that activate K<sup>+</sup> channels that have been proposed as coronary vasodilators for the  
20 treatment of both vasospastic and chronic stable angina.

The availability of multiple K<sup>+</sup> channel subunits allows *in vitro* reconstruction of functional channels, which may comprise different alpha and beta subunits. The individual components may be modified by sequence deletion, substitution, *etc.* to determine the functional role of specific domains.

25 Drug screening may be performed using an *in vitro* model, a genetically altered cell or animal, or purified K<sup>+</sup>Hnov protein, either as monomers, homomultimers or hetermultimers. One can identify ligands or substrates that bind to, modulate or mimic the action of K<sup>+</sup>Hnov. Drug screening identifies agents that provide a replacement for K<sup>+</sup>Hnov function in abnormal cells. Of  
30 particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including



monitoring cellular excitation and conductance, labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, and the like. The purified protein may also be used for determination of three-dimensional crystal structure, which can be used for modeling  
5 intermolecular interactions.

The term "agent" as used herein describes any molecule, e.g. protein or pharmaceutical, with the capability of altering or mimicking the physiological function of *K+Hnov* polypeptide. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the  
10 various concentrations. Typically, one of these concentrations serves as a negative control, i.e. at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate  
15 agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with  
20 one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are  
25 available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds  
30 are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known

pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

Where the screening assay is a binding assay, one or more of the  
5 molecules may be joined to a label, where the label can directly or indirectly provide a detectable signal. Various labels include radioisotopes, fluorescers, chemiluminescers, enzymes, specific binding molecules, particles, *e.g.* magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin *etc.* For the specific binding members,  
10 the complementary member would normally be labeled with a molecule that provides for detection, in accordance with known procedures.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, *e.g.* albumin, detergents, *etc.* that are used to facilitate optimal protein-protein binding and/or reduce non-specific or  
15 background interactions. Reagents that improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.* may be used. The mixture of components are added in any order that provides for the requisite binding. Incubations are performed at any suitable temperature, typically between 4 and 40°C. Incubation periods are selected for optimum  
20 activity, but may also be optimized to facilitate rapid high-throughput screening. Typically between 0.1 and 1 hours will be sufficient.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host in a variety of ways, orally, topically, parenterally *e.g.* subcutaneously, intraperitoneally, by viral  
25 infection, intravascularly, *etc.* Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions,  
30 salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up

compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

It is to be understood that this invention is not limited to the particular methodology, protocols, cell lines, animal species or genera, and reagents described, as such may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

As used herein the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a cell" includes a plurality of such cells and reference to "the cell" includes reference to one or more cells and equivalents thereof known to those skilled in the art, and so forth. All technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs unless clearly indicated otherwise.

It must be noted that as used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a complex" includes a plurality of such complexes and reference to "the formulation" includes reference to one or more formulations and equivalents thereof known to those skilled in the art, and so forth.

All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing, for example, the methods and methodologies that are described in the publications which might be used in connection with the presently described invention. The publications discussed above and throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an

admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention.

#### EXPERIMENTAL

5       The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention. Efforts have been made to ensure accuracy with respect to the numbers used (e.g. amounts, temperature, concentrations, etc.) but some  
10       experimental errors and deviations should be allowed for. Unless otherwise indicated, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees centigrade, and pressure is at or near atmospheric.

#### 15       Methods

Two different types of sequence searches were performed. The first centered on the most highly conserved region of the K<sup>+</sup> channel family, the pore domain. The pore is composed of 15-17 amino acids and can be divided into subfamilies based on the number of transmembrane segments present in the  
20       channel. Eleven variant peptide sequences corresponding to the pore domain were used in TBLASTN searches against the EST division of Genbank. Significant matches were identified, and classified into 2 categories: identical to known human K<sup>+</sup> channels and related to known K<sup>+</sup> channels. The pore sequences are shown in Table 2.

TABLE 2

SEQ ID NO	Genbank #	
49	L02751	TGGTGGGCTGTGGTGACCATGACAACTGTGGGCTATGGGGACATG
50	M60451	TGGTGGGCAGTGGTCACCATGACCACCTGTGGGCTACGGGGACATG
51	L02752	TGGTGGGCAGTCGCTCTCCATGACAACTGTAGGCTATGGAGACATG
52	M55515	TGGTGGGCAGTGGTAACCATGACAACAGTGGGTACGGCGATATG
53	Z11585	TGGTGGGCTGTGGTCACCATGACGACCCCTGGGCTATGGAGACATG
54	U40990	TGGTGGGGGGTGGTCACAGTCACCACCATCGGCTATGGGGACAAG
55	I26643	TGGTGGGCAGTGGTCACCATGACCACGGTGGCTATGGGGACATG
56	M86747	TGGTGGGCCGTGGTCACCATGACGACCCCTGGGCTATGGAGACATG
57	M84876	TGGTGGGCTGTGGTCACCATGACGACACTGGGCTACGGAGACATG
58	M55514	TGGTGGGCTGTGGTGACCATGACAACTGTGGGCTATGGGGACATG
59	X83582	TTCTGTCTCTCCATTGAGACCCGAAACAACCAATTGGGTATGGCTTCCG
60	S78684	TTTTATTCTCAATAGAGACAGAAACCACCATTGGTTATGGCTACCG
61	U22413	TTCTCTCTCTCCATTGAGACCCAGACAACCATAGGCTATGGTTTCAG
62	U24056	TTCTGTCTCTCGGTGGAGACGACGACGACCATCGGCTATGGGTTCCG
63	U52155	TTCTCTCTCTCCCTTGAATCCCAACCACCAATTGGCTATGGCTTCCG
64	D87291	TTCTCTTTTCCCTGGAAATCCCAAGACAACCAATTGGCTATGGAGTCCG
65	D50582	TTCTTTTCTCTCCATTGAGGTCCAAGTACTATTGGCTTTGGGGGCG
66	D50315	TTCTCTCTCTCCATTGAAGTTCAAGTTACCAATTGGGTTTGGAGGGAG
67	U04270	GCGCTCTACTTCACCTTCAGCAGCCCTCACCAGTGTGGGCTTCGGCAAC

The unique pore peptide sequences are shown in Table 3.

TABLE 3

SEQ ID NO	Amino acid sequence
68	WWAVSMTTVGYGDM
69	WWAVTMTTLGYGDM
70	WWGWTVTTIGYGDK
71	WWAVTMTTVGYGDM
72	FLFSIEVQVTIGFGG
73	FLFSLESQTTIGYGV
74	FLFSIETETTIGYGY
75	FLFSIETQTTIGYGF
76	FLFSVETQTTIGYGF
77	FLFSLESQTTIGYGF
78	FLFSIETETTIGYGF
79	ALYFTFSSLTSVGFGN

- 5 The second set of experiments was based on a complex, reiterative process. Annotated protein and DNA sequences were obtained from GenBank for all known K<sup>+</sup> channels from all species. The TBLASTN and BLASTN programs were used to identify homologous ESTs, which were then analyzed using the BLASTX and BLASTN algorithms to identify ESTs which were related to K<sup>+</sup> channels yet not identical to any known human K<sup>+</sup> channel gene.

10 Novel human K<sup>+</sup> channels were defined as those that had clear homology to known K<sup>+</sup> channels from any species and were not present as identities or near identities to any human-derived sequences in any division of Genbank.

- 15 *Isolation of full length cDNA sequence.* EST clones were picked from the IMAGE consortium cDNA library and end-sequenced with vector primers. Gap closure was achieved either by primer walking or transposon sequencing. GeneTrapper (Life

Technologies) was used to isolate larger cDNA clones according to the provided protocol. RACE was used to extend the sequences as necessary using standard protocols.

Sequences were assembled in Sequencher (Gene Codes). The presence of open reading frames was assessed as well as potential start codons. Potential polymorphisms were detected as sequence variants between multiple independent clones. Sequence homologies were detected using the BLAST algorithms.

The completed gene sequences and predicted amino acid sequences are provided as SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21-24, 26 and 28-29. Polymorphisms, chromosome locations and family assignments are shown in Table 1.

ESTs that had top human hits with >95% identity over 100 amino acids were discarded. This was based upon the inventors' experience that these sequences were usually identical to the starting probe sequences, with the differences due to sequence error. The remaining BLASTN and BLASTX outputs for each EST were examined manually, i.e., ESTs were removed from the analysis if the inventors determined that the variation from the known related probe sequence was a result of poor database sequence. Poor database sequence was usually identified as a number of 'N' nucleotides in the database sequence for a BLASTN search and as a base deletion or insertion in the database sequence, resulting in a peptide frameshift, for a BLASTX output. ESTs for which the highest scoring match was to non-related sequences were also discarded at this stage. The EST sequences that correspond to each clone are shown in Table 4.

Table 4

Genbank Accession#	K+Hnov	clone ID	Trace	IMAGE Plate Coordinates	Read 5'/3'
N39619	K+Hnov2	277113	yy51h05.s1	611p10	3'
N46767	K+Hnov2	277113	yy51h05.r1	611p10	5'
R19352	K+Hnov11	33144	yg24f12.r1	155o24	5'
R44628	K+Hnov11	33144	yg24f12.s1	155o24	3'

R35526	K+Hnov14	37299	yg64e08.r1	165o15	5'
R73353	K+Hnov14	157854	yl10e04.r1	251g07	5'
AA397616	K+Hnov14	728558	zt79c08.r1	1787j15	5'
AA286692	K+Hnov28	700757	zs48h03.r1	1715d6	5'
AA150494	K+Hnov42	491748	zl08e07.s1	1170o13	3'
AA156697	K+Hnov42	491748	zl08e07.r1	1170o13	5'
AA191752	K+Hnov42	626699	zp82d06.r1	1522f12	5'
AA216446	K+Hnov42	626699	zp82d06.s1	1522f12	3'
AA430591	K+Hnov42	773611	zw51f10.r1	1904o20	5'
AA236930	K+Hnov44	683888	zs01a05.s1	1671e9	3'
AA236968	K+Hnov44	683888	zs01a05.r1	1671e9	5'

#### EXAMPLE 2: CHROMOSOMAL LOCALIZATION

Two primers were designed in the 3'-untranslated regions of each gene sequence to amplify a product across the Stanford G3 radiation hybrid map, or the Whitehead GB4 panel. The PCR data were submitted for automatic two-point analysis. Mapping data were correlated with cytoband information and comparisons with the OMIM human gene map data base were made. The following primers were made:

- 10 K+Hnov1 on GB4  
(SEQ ID NO:31) F: 5' TATCCACATCAATGGACAAAGC 3'  
(SEQ ID NO:32) R: 5' TGCATAACTGGCTGGGTGTA 3'  
Results: 1.71 cR from D2S331, Cytogenetic location of 2q37
- 15 K+Hnov2 on G3  
F: 5' GTCAGGTGACCGAGTTCA 3'  
R: 5' GCTCCATCTCCAGATTCTTC 3'  
Results: 0.0 cR from SHGC-1320, Cytogenetic location of 11q12
- 20 K+Hnov6 on GB4  
(SEQ ID NO:33) F: 5' TGACATCACTGGATGAACTTGA 3'  
(SEQ ID NO:34) R: 5' TGCCTGCAAAGTTTGAACAT 3'  
Results: 5.23 cR from WI-5509, Cytogenetic location of 2p23
- 25 K+Hnov9 on GB4  
(SEQ ID NO:35) F: 5' TGACATCACTGGATGAACTTGA 3'  
(SEQ ID NO:36) R: 5' TGCCTGCAAAGTTTGAACAT 3'



Results: 1.21 cR from AFM200VC7, Cytogenetic location of 8q23

K+Hnov11 on GB4

(SEQ ID NO:37) F: 5' ACCTGGTGGTATGGAAGCAT 3'

5 (SEQ ID NO:38) R: 5' TTTCTCCTGGCCTCTACCC 3'

Results: 2.43 cR from WI-6756, Cytogenetic location of 8q23

K+Hnov12 on G3

(SEQ ID NO:39) F: 5' TCCCTCTTGGGTGACCTTC 3'

10 (SEQ ID NO:40) R: 5' ATCTTTGTGACCCACCAGCT 3'

Results: 7.45 cR from SHGC-32925, Cytogenetic location of Xp21

K+Hnov14 on GB4

(SEQ ID NO:41) F: 5' AGGTGTGCTGCCATCTGCTGTTGCG 3'

15 (SEQ ID NO:42) R: 5' AGCCTATCCTCTCTGAGAGTCAGG

Results: 7.69 cR from WI-7107, Cytogenetic location of 12q14

K+Hnov28 on GB4

(SEQ ID NO:43) F: 5' AAGCAGAGTACTCATGATGCC 3'

20 (SEQ ID NO:44) R: 5' TCTGGTAGACAGTACAGTGG 3'

Results: 35.38 cR from WI-9695, Cytogenetic location of 3q29

K+Hnov42 on G3

(SEQ ID NO:45) F: 5' CATTTGGCTGGTCCAAGATG 3'

25 (SEQ ID NO:46) R: 5' AGTCATTGGTAGGGAGGTAC 3'

Results: 7.45 cR from SHGC-32925, Cytogenetic location of Xp21

K+Hnov44 on G3

(SEQ ID NO:47) F: 5' CATGCTTCTACAGTCCAGCC 3'

30 (SEQ ID NO:48) R: 5' GGTCTCAGTTGCAGAAATC 3'

Results: 7.45 cR from SHGC-32925, Cytogenetic location of Xp21

Map positions for K+Hnov15 and K+Hnov27 were obtained from public databases.

K+Hnov2 and K+Hnov4 have not been mapped.

35

### EXAMPLE 3: EXPRESSION ANALYSIS

RT-PCR was utilized to characterize the expression pattern of the novel ion channels. This approach used RNA from 30 different tissues to generate first strand cDNA. Total RNA was purchased (Clontech, Invitrogen) and used to synthesize first strand cDNA using M-MLV reverse transcriptase and the supplied buffer (Gibco-BRL). The 20 µl reaction contained 5 µg total RNA, 100 ng of random primers, 10 mM DTT.

0.5 mM each dNTP, and an RNase inhibitor (Gibco-BRL). Identical reactions were set up without reverse transcriptase to control for DNA contamination in the RNA samples. The synthesis reaction proceeded for 1 hour at 37°C followed by 10 minutes at 95°C. These cDNAs, along with control cDNA synthesis reactions without reverse transcriptase, were diluted 1:5 and 2 µl of each sample were arrayed into 96-well trays, dried, and resuspended in PCR buffer prior to PCR amplification. The cDNAs were tested with primers with defined expression patterns to verify the presence of amplifiable cDNA from each tissue. Gene-specific primers were used to amplify the cDNAs in 20 µl PCR reactions with standard conditions, 2.5 mM MgCl<sub>2</sub>, Taq Gold, and an appropriate annealing temperature.

This approach provides for relatively high-throughput analysis of gene expression in a large set of tissues in a cost-efficient manner and provides qualitative analysis of gene expression only. Modifications can be employed, such as the use of internal control primers, limited cycling parameters, and dilution series to convert this to a quantitative experiment.

[illegible]

A "+" indicates expression in the tissue, a "-" indicates no expression, and blank square indicates no data for that sample.

**K+Hnov49 on Whitehead GB4 RH mapping panel:**

Primer 1 (SEQ ID NO:5): 5' - CATAGCCATAGGTGAGGACT - 3'

Primer 2: (SEQ ID NO:6) 5' - GAGAGGAAAACAGTCTGGGC - 3'

5 Results: Cytogenetic location 1q41, 4.6cR from framework marker D1S217

**K+Hnov59 on Whitehead GB4 RH mapping panel**

Primer 1 (SEQ ID NO:7): 5' - GGACATCGAACTAAGACCTG - 3'

Primer 2 (SEQ ID NO:8): 5' - TCCCATGCCATTTCAGATCTG - 3'

10 Results: Cytogenetic location 19q13.2, 8.34cR from framework marker D19S425

**EXPRESSION ANALYSIS OF K+HNOV49**

A probe was created from a fragment corresponding to nucleotides 50 to 1284 of SEQ ID NO:83 (K+Hnov49) and purified DNA fragment was labeled with  
15 [<sup>32</sup>P]dCTP (Amersham) by the random primer method. Adult human Multiple Tissue Northern (MTM™) Blots (Clontech) were hybridized with the [<sup>32</sup>P]-labeled fragment in ExpressHyb™ solution (Clontech) for four hours, washed to a final stringency of 0.1xSSC, 0.1% SDS at 65°C and subjected to autoradiography for 24 hours.

20 Analysis revealed that K+Hnov49 is expressed as an approximately 4.2kb mRNA. Expression levels of K+Hnov49 are high in brain and liver and low in kidney tissues. No mRNA was detectable on these Northern blots for heart, skeletal muscle, colon, thymus, spleen, small intestine, placenta, lung or peripheral blood leukocytes indicating either a very low level of expression or that  
25 it is not expressed in these tissues. Expression analysis was also carried out by RT-PCR across an extended series of tissues. The results of these analyses are shown in Table 4. Primer pairs used for amplification of K+Hnov49 and 59 are the same as those used for RH mapping as indicated above.

Table 4

	Adipose	Adrenal Gland	Bladder	Brain	Cerebellum	Cervix	Colon	Esophagus	Fetal Brain	Fetal Liver	Heart	HeLa Cell	Kidney	Liver	Lung	Mammary Gland	Pancreas	Placenta	Prostate	Rectum	Salivary Gland	Skeletal Muscle	Skin	Small Intestine	Spleen	Stomach	Testis	Thymus	Trachea	Uterus
#1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
#2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

## WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding a mammalian K+Hnov protein.
2. An isolated nucleic acid according to Claim 1, wherein said K+Hnov  
5 protein has the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18,  
20, 25, 27, 30, 81 or 83.
3. An isolated nucleic acid according to Claim 1, wherein said K+Hnov  
10 protein has an amino acid sequence that is substantially identical to the amino  
acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 25, 27, 30, 81 or  
83.
4. An isolated nucleic acid according to Claim 1 wherein the nucleotide  
15 sequence of said nucleic acid is SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21,  
22, 23, 24, 26, 28, 29, 80 or 82.
5. An isolated nucleic acid that hybridizes under stringent conditions to  
a nucleic acid sequence of claim 4.
- 20 6. An expression cassette comprising a transcriptional initiation region  
functional in an expression host, a nucleic acid having a sequence of the isolated  
nucleic acid according to Claim 1 under the transcriptional regulation of said  
transcriptional initiation region, and a transcriptional termination region functional  
in said expression host.
- 25 7. A cell comprising an expression cassette according to Claim 6 as  
part of an extrachromosomal element or integrated into the genome of a host cell  
as a result of introduction of said expression cassette into said host cell, and the  
cellular progeny of said host cell.
- 30

8. A method for producing mammalian K+Hnov protein, said method comprising:

growing a cell according to Claim 7, whereby said mammalian K+Hnov protein is expressed; and

5 isolating said K+Hnov protein free of other proteins.

9. A purified polypeptide composition comprising at least 50 weight % of the protein present as a K+Hnov protein or a fragment thereof.

10. A monoclonal antibody binding specifically to a K+Hnov protein.

11. A non-human transgenic animal model for K+Hnov gene function wherein said transgenic animal comprises an introduced alteration in a K+Hnov gene.

15

12. The animal model of claim 11, wherein said animal is heterozygous for said introduced alteration.

13. The animal model of claim 12, wherein said animal is homozygous  
20 for said introduced alteration.

14. The animal model of claim 12, wherein said introduced alteration is a knockout of endogenous K+Hnov gene expression.

## SEQUENCE LISTING

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Buckler, Alan

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 Thr Tyr Arg Ser Thr Leu Arg Thr Leu Pro Gly Thr Arg Leu Ala Trp  
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 Leu Ala Asp Pro Asp Gly Gly Gly Arg Pro Glu Thr Asp Gly Gly Gly  
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Val Gly Ser Ser Gly Ser Ser Gly Gly Gly Cys Glu Phe Phe Phe	
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Asp Arg His Pro Gly Val Phe Ala Tyr Val Leu Asn Tyr Tyr Arg Thr	
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Gly Lys Leu His Cys Pro Ala Asp Val Cys Gly Pro Leu Phe Glu Glu	
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Glu Leu Ala Phe Trp Gly Ile Asp Glu Thr Asp Val Glu Pro Cys Cys	
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Trp Met Thr Tyr Arg Gln His Arg Asp Ala Glu Glu Ala Leu Asp Ile	
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Pro Asp Gly Lys Ser Gly Arg Trp Arg Arg Leu Gln Pro Arg Met Trp	
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Ala Leu Phe Glu Asp Pro Tyr Ser Ser Arg Ala Ala Arg Phe Ile Ala	
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Phe Ala Ser Leu Phe Phe Ile Leu Val Ser Ile Thr Thr Phe Cys Leu	
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Glu Thr His Glu Ala Phe Asn Ile Val Lys Asn Lys Thr Glu Pro Val	
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atc aat ggc aca agt gtt gtt cta cag tat gaa att gaa acg gat cct	836
Ile Asn Gly Thr Ser Val Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro	
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Ala Leu Thr Tyr Val Glu Gly Val Cys Val Val Trp Phe Thr Phe Glu	
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Phe Leu Val Arg Ile Val Phe Ser Pro Asn Lys Leu Glu Phe Ile Lys	
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Asn Leu Leu Asn Ile Ile Asp Phe Val Ala Ile Leu Pro Phe Tyr Leu	
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gag gtg gga ctc agt ggc ctg tca tcc aaa gct gct aaa gat gtg ctt	1028

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Gly	Phe	Leu	Arg	Val	Val	Arg	Phe	Val	Arg	Ile	Leu	Arg	Ile	Phe	Lys		
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ctc	acc	cgc	cat	ttt	gta	ggt	ctg	agg	gtg	ctt	gga	cat	act	ctt	cga		1124
Leu	Thr	Arg	His	Phe	Val	Gly	Leu	Arg	Val	Leu	Gly	His	Thr	Leu	Arg		
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gct	agt	act	aat	gaa	ttt	ttg	ctg	ctg	ata	att	ttc	ctg	gct	cta	gga		1172
Ala	Ser	Thr	Asn	Glu	Phe	Leu	Leu	Leu	Ile	Ile	Phe	Leu	Ala	Leu	Gly		
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Val	Leu	Ile	Phe	Ala	Thr	Met	Ile	Tyr	Tyr	Ala	Glu	Arg	Val	Gly	Ala		
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caa	cct	aac	gac	cct	tca	gct	agt	gag	cac	aca	cag	ttc	aaa	aac	att		1268
Gln	Pro	Asn	Asp	Pro	Ser	Ala	Ser	Glu	His	Thr	Gln	Phe	Lys	Asn	Ile		
		375					380					385					
ccc	att	ggg	ttc	tgg	tgg	gct	gta	gtg	acc	atg	act	acc	ctg	ggt	tat		1316
Pro	Ile	Gly	Phe	Trp	Trp	Ala	Val	Val	Thr	Met	Thr	Thr	Leu	Gly	Tyr		
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Gly	Asp	Met	Tyr	Pro	Gln	Thr	Trp	Ser	Gly	Met	Leu	Val	Gly	Ala	Leu		
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Cys	Ala	Leu	Ala	Gly	Val	Leu	Thr	Ile	Ala	Met	Pro	Val	Pro	Val	Ile		
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Val	Asn	Asn	Phe	Gly	Met	Tyr	Tyr	Ser	Leu	Ala	Met	Ala	Lys	Gln	Lys		
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ctt	cca	agg	aaa	aga	aag	aag	cac	atc	cct	cct	gct	cct	cag	gca	agc		1508
Leu	Pro	Arg	Lys	Arg	Lys	Lys	His	Ile	Pro	Pro	Ala	Pro	Gln	Ala	Ser		
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Ser	Pro	Thr	Phe	Cys	Lys	Thr	Glu	Leu	Asn	Met	Ala	Cys	Asn	Ser	Thr		
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cag	agt	gac	aca	tgt	ctg	ggc	aaa	gac	aat	cga	ctt	ctg	gaa	cat	aac		1604
Gln	Ser	Asp	Thr	Cys	Leu	Gly	Lys	Asp	Asn	Arg	Leu	Leu	Glu	His	Asn		
	485				490				495					500			
aga	tca	gtg	tta	tca	ggt	gac	gac	agt	aca	gga	agt	gag	ccg	cca	cta		1652
Arg	Ser	Val	Leu	Ser	Gly	Asp	Asp	Ser	Thr	Gly	Ser	Glu	Pro	Pro	Leu		
			505					510					515				
tca	ccc	cca	gaa	agg	ctc	ccc	atc	aga	cgc	tct	agt	acc	aga	gac	aaa		1700
Ser	Pro	Pro	Glu	Arg	Leu	Pro	Ile	Arg	Arg	Ser	Ser	Thr	Arg	Asp	Lys		
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aac	aga	aga	ggg	gaa	aca	tgt	ttc	cta	ctg	acg	aca	ggt	gat	tac	acg		1748
Asn	Arg	Arg	Gly	Glu	Thr	Cys	Phe	Leu	Leu	Thr	Thr	Gly	Asp	Tyr	Thr		

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 Val Thr Ser Pro Tyr Asn Ser Pro Cys Pro Leu Arg Arg Ser Arg Ser  
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 Pro Ile Pro Ser Ile  
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 20                      25                      30  
 Arg Leu Ala Trp Leu Ala Asp Pro Asp Gly Gly Gly Arg Pro Glu Thr  
 35                      40                      45  
 Asp Gly Gly Gly Val Gly Ser Ser Gly Ser Ser Gly Gly Gly Gly Cys  
 50                      55                      60  
 Glu Phe Phe Phe Asp Arg His Pro Gly Val Phe Ala Tyr Val Leu Asn  
 65                      70                      75                      80  
 Tyr Tyr Arg Thr Gly Lys Leu His Cys Pro Ala Asp Val Cys Gly Pro  
 85                      90                      95  
 Leu Phe Glu Glu Glu Leu Ala Phe Trp Gly Ile Asp Glu Thr Asp Val  
 100                      105                      110  
 Glu Pro Cys Cys Trp Met Thr Tyr Arg Gln His Arg Asp Ala Glu Glu  
 115                      120                      125  
 Ala Leu Asp Ile Phe Glu Thr Pro Asp Leu Ile Gly Gly Asp Pro Gly  
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 Asp Asp Glu Asp Leu Ala Lys Arg Leu Gly Ile Glu Asp Ala Ala  
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 Gly Leu Gly Gly Pro Asp Gly Lys Ser Gly Arg Trp Arg Arg Leu Gln  
 165                      170                      175  
 Pro Arg Met Trp Ala Leu Phe Glu Asp Pro Tyr Ser Ser Arg Ala Ala  
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 Arg Phe Ile Ala Phe Ala Ser Leu Phe Phe Ile Leu Val Ser Ile Thr  
 195                      200                      205  
 Thr Phe Cys Leu Glu Thr His Glu Ala Phe Asn Ile Val Lys Asn Lys  
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 Thr Glu Pro Val Ile Asn Gly Thr Ser Val Val Leu Gln Tyr Glu Ile  
 225                      230                      235                      240  
 Glu Thr Asp Pro Ala Leu Thr Tyr Val Glu Gly Val Cys Val Val Trp  
 245                      250                      255  
 Phe Thr Phe Glu Phe Leu Val Arg Ile Val Phe Ser Pro Asn Lys Leu  
 260                      265                      270  
 Glu Phe Ile Lys Asn Leu Leu Asn Ile Ile Asp Phe Val Ala Ile Leu  
 275                      280                      285

Pro Phe Tyr Leu Glu Val Gly Leu Ser Gly Leu Ser Ser Lys Ala Ala  
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 Lys Asp Val Leu Gly Phe Leu Arg Val Val Arg Phe Val Arg Ile Leu  
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 Arg Ile Phe Lys Leu Thr Arg His Phe Val Gly Leu Arg Val Leu Gly  
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 His Thr Leu Arg Ala Ser Thr Asn Glu Phe Leu Leu Leu Ile Phe  
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 Thr Leu Gly Tyr Gly Asp Met Tyr Pro Gln Thr Trp Ser Gly Met Leu  
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 Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile Arg Arg Ser Ser  
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 Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe Leu Leu Thr Thr  
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 Gly Asp Tyr Thr Cys Ala Ser Asp Gly Gly Ile Arg Lys Gly Tyr Glu  
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 Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala Gly Asn Ala Leu  
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&lt;210&gt; 5

&lt;211&gt; 2293

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

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&lt;222&gt; (330)... (1800)

&lt;223&gt; K+Hnov6

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 Met Val Phe Gly Glu Phe Phe His  
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aag cag tct gtt gac caa agc acc ctc ctg cgg ttt cct cac acc aga Lys Gln Ser Val Asp Gln Ser Thr Leu Leu Arg Phe Pro His Thr Arg 25 30 35 40	449
ctg ggg aag ctg ctt act tgc cat tct gaa gag gcc att ctg gag ctg Leu Gly Lys Leu Leu Thr Cys His Ser Glu Glu Ala Ile Leu Glu Leu 45 50 55	497
tgt gat gat tac agt gtg gcc gat aag gaa tac tac ttt gat cgg aat Cys Asp Asp Tyr Ser Val Ala Asp Lys Glu Tyr Tyr Phe Asp Arg Asn 60 65 70	545
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cat gtc atg gag gag ctg tgc gta ttc tca ttc tgc cag gag atc gag His Val Met Glu Glu Leu Cys Val Phe Ser Phe Cys Gln Glu Ile Glu 90 95 100	641
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aaa ttc tgg aaa aac cct ctg aac atc att gac ttt gtc tct att att	1121



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Pro	Phe	Tyr	Ala	Thr	Leu	Ala	Val	Asp	Thr	Lys	Glu	Glu	Glu	Ser	Glu	
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Asp	Ile	Glu	Asn	Met	Gly	Lys	Val	Val	Gln	Ile	Leu	Arg	Leu	Met	Arg	
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Ile	Phe	Arg	Ile	Leu	Lys	Leu	Ala	Arg	His	Ser	Val	Gly	Leu	Arg	Ser	
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Trp	Trp	Trp	Ala	Thr	Ile	Ser	Met	Thr	Val	Gly	Tyr	Gly	Asp	Thr		
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Cys	Gly	Ile	Leu	Val	Val	Ala	Leu	Pro	Ile	Thr	Ile	Ile	Phe	Asn	Lys	
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Phe	Ser	Lys	Tyr	Tyr	Gln	Lys	Gln	Lys	Asp	Ile	Asp	Val	Asp	Gln	Cys	
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Arg	Asp	Ile	Tyr	Ala	Gln	Arg	Met	His	Ala	Phe	Ile	Thr	Ser	Leu	Ser	
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Ser	Val	Gly	Ile	Val	Val	Ser	Asp	Pro	Asp	Ser	Thr	Asp	Ala	Ser	Ser	
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Ile	Glu	Asp	Asn	Glu	Asp	Ile	Cys	Asn	Thr	Thr	Ser	Leu	Glu	Asn	Cys	
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aca	gca	a	aat	gag	cggg	ggg	gttt	gtg	cct	gttt	ctc	ttat	ccttt	cca	acattag	1850
Thr	Ala															

490

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&lt;210&gt; 6

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 6

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Lys Glu Tyr Tyr Phe Asp Arg Asn Pro Ser Leu Phe Arg Tyr Val Leu
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Asn Phe Tyr Tyr Thr Gly Lys Leu His Val Met Glu Glu Leu Cys Val
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Phe Ser Phe Cys Gln Glu Ile Glu Tyr Trp Gly Ile Asn Glu Leu Phe
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Ile Asp Ser Cys Cys Ser Asn Arg Tyr Gln Glu Arg Lys Glu Glu Asn
115      120      125
His Glu Lys Asp Trp Asp Gln Lys Ser His Asp Val Ser Thr Asp Ser
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Asn Pro Ala Tyr Cys Leu Ser Ala Lys Leu Ile Ala Ile Ser Ser Leu
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Ser Val Val Leu Ala Ser Ile Val Ala Met Cys Val His Ser Met Ser
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Ile Ile Asp Phe Val Ser Ile Ile Pro Phe Tyr Ala Thr Leu Ala Val
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Asp Thr Lys Glu Glu Glu Ser Glu Asp Ile Glu Asn Met Gly Lys Val
275      280      285
Val Gln Ile Leu Arg Leu Met Arg Ile Phe Arg Ile Leu Lys Leu Ala
290      295      300
Arg His Ser Val Gly Leu Arg Ser Leu Gly Ala Thr Leu Arg His Ser
305      310      315      320
Tyr His Glu Val Gly Leu Leu Leu Leu Phe Leu Ser Val Gly Ile Ser
325      330      335
Ile Phe Ser Val Leu Ile Tyr Ser Val Glu Lys Asp Asp His Thr Ser
340      345      350

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Ser Leu Thr Ser Ile Pro Ile Cys Trp Trp Trp Ala Thr Ile Ser Met  
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 370 375 380  
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 385 390 395 400  
 Pro Ile Thr Ile Ile Phe Asn Lys Phe Ser Lys Tyr Tyr Gln Lys Gln  
 405 410 415  
 Lys Asp Ile Asp Val Asp Gln Cys Ser Glu Asp Ala Pro Glu Lys Cys  
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 His Glu Leu Pro Tyr Phe Asn Ile Arg Asp Ile Tyr Ala Gln Arg Met  
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 His Ala Phe Ile Thr Ser Leu Ser Ser Val Gly Ile Val Val Ser Asp  
 450 455 460  
 Pro Asp Ser Thr Asp Ala Ser Ser Ile Glu Asp Asn Glu Asp Ile Cys  
 465 470 475 480  
 Asn Thr Thr Ser Leu Glu Asn Cys Thr Ala  
 485 490

&lt;210&gt; 7

&lt;211&gt; 3080

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (480)...(1977)

&lt;223&gt; K+Hnov9

&lt;400&gt; 7

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 Met Pro Ser Ser Gly Arg Ala Leu Leu Asp Ser Pro Leu Asp Ser Gly  
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 Ser Leu Thr Ser Leu Asp Ser Ser Val Phe Cys Ser Glu Gly Glu Gly  
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 gag ccc ttg gcg ctc ggg gac tgc ttc acg gtc aac gtg ggc ggc agc 623  
 Glu Pro Leu Ala Leu Gly Asp Cys Phe Thr Val Asn Val Gly Gly Ser  
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 cgc ttc gtg ctc tgc cag cag gcg ctg tcc tgc ttc ccg cac acg cgc 671  
 Arg Phe Val Leu Ser Gln Gln Ala Leu Ser Cys Phe Pro His Thr Arg  
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 ctt ggc aag ctg gcc gtg gtg gtg gct tcc tac cgc cgc ccc ggg gcc 719  
 Leu Gly Lys Leu Ala Val Val Val Ala Ser Tyr Arg Arg Pro Gly Ala  
 65 70 75 80  
 ctg gcc gcc gtg ccc agc cct ctg gag ctt tgc gac gat gcc aac ccc 767  
 Leu Ala Ala Val Pro Ser Pro Leu Glu Leu Cys Asp Asp Ala Asn Pro  
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Val Asp Asn Glu Tyr Phe Phe Asp Arg Ser Ser Gln Ala Phe Arg Tyr	
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gtc ctg cac tac tac cgc acc ggc cgc ctg cat gtc atg gag cag ctg	863
Val Leu His Tyr Tyr Arg Thr Gly Arg Leu His Val Met Glu Gln Leu	
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Cys Ala Leu Ser Phe Leu Gln Glu Ile Gln Tyr Trp Gly Ile Asp Glu	
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ctc agc atc gat tcc tgc tgc agg gac aga tac ttc aga agg aaa gag	959
Leu Ser Ile Asp Ser Cys Cys Arg Asp Arg Tyr Phe Arg Arg Lys Glu	
145 150 155 160	
ctg agt gaa act tta gac ttc aag aag gac aca gaa gac cag gaa agt	1007
Leu Ser Glu Thr Leu Asp Phe Lys Lys Asp Thr Glu Asp Gln Glu Ser	
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Gln His Glu Ser Glu Gln Asp Phe Ser Gln Gly Pro Cys Pro Thr Val	
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cgc cag aag ctc tgg aat atc ctg gag aaa cct gga tct tcc aca gct	1103
Arg Gln Lys Leu Trp Asn Ile Leu Glu Lys Pro Gly Ser Ser Thr Ala	
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Ala Arg Ile Phe Gly Val Ile Ser Ile Ile Phe Val Val Val Ser Ile	
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Ile Asn Met Ala Leu Met Ser Ala Glu Leu Ser Trp Leu Asp Leu Gln	
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ctg ctg gaa atc ctg gag tat gtg tgc att agc tgg ttc acc ggg gag	1247
Leu Leu Glu Ile Leu Glu Tyr Val Cys Ile Ser Trp Phe Thr Gly Glu	
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Phe Val Leu Arg Phe Leu Cys Val Arg Asp Arg Cys Arg Phe Leu Arg	
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aag gtg cca aac atc ata gac ctc ctt gcc atc ttg ccc ttc tac atc	1343
Lys Val Pro Asn Ile Ile Asp Leu Leu Ala Ile Leu Pro Phe Tyr Ile	
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act ctt ctg gta gag agc cta agt ggg agc cag acc acg cag gag ctg	1391
Thr Leu Leu Val Glu Ser Leu Ser Gly Ser Gln Thr Thr Gln Glu Leu	
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gag aac gtg ggg cgc att gtc cag gtg ttg agg ctg ctc agg gct ctg	1439
Glu Asn Val Gly Arg Ile Val Gln Val Leu Arg Leu Leu Arg Ala Leu	
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cgc atg cta aag ctg ggc aga cat tcc aca gga tta cgc tcc ctt ggg	1487
Arg Met Leu Lys Leu Gly Arg His Ser Thr Gly Leu Arg Ser Leu Gly	
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 Met Thr Ile Thr Gln Cys Tyr Glu Glu Val Gly Leu Leu Leu Leu Phe  
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cta tcc gtg gga atc tct ata ttt tca act gta gaa tac ttt gct gag 1583  
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 Gln Ser Ile Pro Asp Thr Thr Phe Thr Ser Val Pro Cys Ala Trp Trp  
 370 375 380

tgg gcc acc acc tct atg act act gtg gga tat ggg gac att aga cca 1679  
 Trp Ala Thr Thr Ser Met Thr Thr Val Gly Tyr Gly Asp Ile Arg Pro  
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gac acc acc aca ggc aaa atc gtg gcc ttc atg tgt ata tta tgc gga 1727  
 Asp Thr Thr Thr Gly Lys Ile Val Ala Phe Met Cys Ile Leu Ser Gly  
 405 410 415

att ctt gtc ttg gcc ttg cct att gct att att aac gat cgc ttc tct 1775  
 Ile Leu Val Leu Ala Leu Pro Ile Ala Ile Ile Asn Asp Arg Phe Ser  
 420 425 430

gct tgc tac ttc acc ttg aaa ctc aag gaa gca gct gtt aga cag cgt 1823  
 Ala Cys Tyr Phe Thr Leu Lys Leu Lys Glu Ala Ala Val Arg Gln Arg  
 435 440 445

gaa gcc cta aag aag ctt acc aag aat ata gcc act gac tca tat atc 1871  
 Glu Ala Leu Lys Lys Leu Thr Lys Asn Ile Ala Thr Asp Ser Tyr Ile  
 450 455 460

agt gtt aac ttg aga gat gtc tat gcc cgg agt atc atg gag atg ctg 1919  
 Ser Val Asn Leu Arg Asp Val Tyr Ala Arg Ser Ile Met Glu Met Leu  
 465 470 475 480

cga ctg aaa ggc aga gaa aga gca agt act agg agc agc ggg gga gat 1967  
 Arg Leu Lys Gly Arg Glu Arg Ala Ser Thr Arg Ser Ser Gly Gly Asp  
 485 490 495

gat ttc tgg t tttgaattaa ttttcaattt atttacaata gctatgtaca 2017  
 Asp Phe Trp

attaactaaa atgataaagc agtgatgtgg atttctgtat tctgatgatg agtctcttca 2077  
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 atgtaaaagt gaggtagtga acatcctaaa tttctacact ggaattacta aataatctta 2857  
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 ttgttaacaa aaaaatacta tggacagctt tctgattgtt ggggtaata gcaaatgttc 2977  
 aaactttgca ggcattttga cattcatcat aacaacacaa ttcctagaca ttgtattata 3037

taattaaagc caaaacctct aaagctaaaa aaaaaaaaaa aaa

3080

&lt;210&gt; 8

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 8

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 Ser Leu Thr Ser Leu Asp Ser Ser Val Phe Cys Ser Glu Gly Glu Gly  
 20 25 30  
 Glu Pro Leu Ala Leu Gly Asp Cys Phe Thr Val Asn Val Gly Gly Ser  
 35 40 45  
 Arg Phe Val Leu Ser Gln Gln Ala Leu Ser Cys Phe Pro His Thr Arg  
 50 55 60  
 Leu Gly Lys Leu Ala Val Val Val Ala Ser Tyr Arg Arg Pro Gly Ala  
 65 70 75 80  
 Leu Ala Ala Val Pro Ser Pro Leu Glu Leu Cys Asp Asp Ala Asn Pro  
 85 90 95  
 Val Asp Asn Glu Tyr Phe Phe Asp Arg Ser Ser Gln Ala Phe Arg Tyr  
 100 105 110  
 Val Leu His Tyr Tyr Arg Thr Gly Arg Leu His Val Met Glu Gln Leu  
 115 120 125  
 Cys Ala Leu Ser Phe Leu Gln Glu Ile Gln Tyr Trp Gly Ile Asp Glu  
 130 135 140  
 Leu Ser Ile Asp Ser Cys Cys Arg Asp Arg Tyr Phe Arg Arg Lys Glu  
 145 150 155 160  
 Leu Ser Glu Thr Leu Asp Phe Lys Lys Asp Thr Glu Asp Gln Glu Ser  
 165 170 175  
 Gln His Glu Ser Glu Gln Asp Phe Ser Gln Gly Pro Cys Pro Thr Val  
 180 185 190  
 Arg Gln Lys Leu Trp Asn Ile Leu Glu Lys Pro Gly Ser Ser Thr Ala  
 195 200 205  
 Ala Arg Ile Phe Gly Val Ile Ser Ile Ile Phe Val Val Val Ser Ile  
 210 215 220  
 Ile Asn Met Ala Leu Met Ser Ala Glu Leu Ser Trp Leu Asp Leu Gln  
 225 230 235 240  
 Leu Leu Glu Ile Leu Glu Tyr Val Cys Ile Ser Trp Phe Thr Gly Glu  
 245 250 255  
 Phe Val Leu Arg Phe Leu Cys Val Arg Asp Arg Cys Arg Phe Leu Arg  
 260 265 270  
 Lys Val Pro Asn Ile Ile Asp Leu Leu Ala Ile Leu Pro Phe Tyr Ile  
 275 280 285  
 Thr Leu Leu Val Glu Ser Leu Ser Gly Ser Gln Thr Thr Gln Glu Leu  
 290 295 300  
 Glu Asn Val Gly Arg Ile Val Gln Val Leu Arg Leu Leu Arg Ala Leu  
 305 310 315 320  
 Arg Met Leu Lys Leu Gly Arg His Ser Thr Gly Leu Arg Ser Leu Gly  
 325 330 335  
 Met Thr Ile Thr Gln Cys Tyr Glu Glu Val Gly Leu Leu Leu Phe  
 340 345 350  
 Leu Ser Val Gly Ile Ser Ile Phe Ser Thr Val Glu Tyr Phe Ala Glu  
 355 360 365  
 Gln Ser Ile Pro Asp Thr Thr Phe Thr Ser Val Pro Cys Ala Trp Trp  
 370 375 380  
 Trp Ala Thr Thr Ser Met Thr Thr Val Gly Tyr Gly Asp Ile Arg Pro  
 385 390 395 400  
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 405 410 415  
 Ile Leu Val Leu Ala Leu Pro Ile Ala Ile Ile Asn Asp Arg Phe Ser

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cccaccatcc	tggagacagc	cacattctcc	taaagccac	cctcactaag	tctccctggg		240								
cttggggagt	ggcacg atg	gcg gca ggc	ctg gcc acg	tgg ctg cct	ttt gct		292								
	Met	Ala Ala Gly	Leu Ala Thr	Trp Leu Pro	Phe Ala										
	1		5		10										
egg gca gca gca gtg ggc tgg ctg ccc ccg gcc cag caa ccc ctg ccc							340								
Arg Ala Ala Ala Val Gly Trp Leu Pro Pro Ala Gln Gln Pro Leu Pro															
	15		20		25										
ccg gca ccg ggg gtg aag gca tct cga gga gat grg gtt ctg gtg gtg							388								
Pro Ala Pro Gly Val Lys Ala Ser Arg Gly Asp Xaa Val Leu Val Val															
	30		35		40										
aac gtg agc gga cgg cgc ttt gag act tgg aag aat acg ctg gac cgc							436								
Asn Val Ser Gly Arg Arg Phe Glu Thr Trp Lys Asn Thr Leu Asp Arg															
	45		50		55		60								
tac.cca gac acc ttg ctg ggc agc tcg gag aag gaa ttc ttc tac gat							484								
Tyr Pro Asp Thr Leu Leu Gly Ser Ser Glu Lys Glu Phe Phe Tyr Asp															
	65		70		75										
gct gac tca ggc gag tac ttc ttc gat cgc gac cct gac atg ttc cgc							532								
Ala Asp Ser Gly Glu Tyr Phe Phe Asp Arg Asp Pro Asp Met Phe Arg															
	80		85		90										
dat gtg ctg aac ttc tac cga acg ggg cgg ctg cat tgc cca cgg cag							580								
His Val Leu Asn Phe Tyr Arg Thr Gly Arg Leu His Cys Pro Arg Gln															
	95		100		105										
gag tgc atc cag gcc ttc gac gaa gag ctg gct ttc tac ggc ctg gtt							628								
Glu Cys Ile Gln Ala Phe Asp Glu Glu Leu Ala Phe Tyr Gly Leu Val															
	110		115		120										
ccc gag cta gtc ggt gac tgc tgc ctt gaa gag tat cgg gac cga aag							676								
Pro Glu Leu Val Gly Asp Cys Cys Leu Glu Glu Tyr Arg Asp Arg Lys															

125		130		135		140	
aag gag aat gdc gag cgc ctg gca gag gat gag gag gca gag cad gcc							724
Lys Glu Asn Ala Glu Arg Leu Ala Glu Asp Glu Glu Ala Glu Gln Ala							
	145			150		155	
ggg gac ggc cca gcc ctg cca gca ggc agc tcc ctg cgg cag cgg ctc							772
Gly Asp Gly Pro Ala Leu Pro Ala Gly Ser Ser Leu Arg Gln Arg Leu							
	160			165		170	
tgg cgg gcc ttc gag aat cca cac acg agc acc gca gcc ctc gtt ttc							820
Trp Arg Ala Phe Glu Asn Pro His Thr Ser Thr Ala Ala Leu Val Phe							
	175			180		185	
tac tat gtg acc ggc ttc ttc atc gcc gtg tgc gtc atc gcc aat gtg							868
Tyr Tyr Val Thr Gly Phe Phe Ile Ala Val Ser Val Ile Ala Asn Val							
	190			195		200	
gtg gag acc atc cca tgc cgc ggc tct gca cgc agg tcc tca agg gag							916
Val Glu Thr Ile Pro Cys Arg Gly Ser Ala Arg Arg Ser Ser Arg Glu							
	205			210		215	220
cag ccc tgt ggc gaa cgc ttc cca cag gcc ttt ttc tgc atg gac aca							964
Gln Pro Cys Gly Glu Arg Phe Pro Gln Ala Phe Phe Cys Met Asp Thr							
	225			230		235	
gcc tgt gta ctc ata ttc aca ggt gaa tac ctc ctg cgg ctg ttt gcc							1012
Ala Cys Val Leu Ile Phe Thr Gly Glu Tyr Leu Leu Arg Leu Phe Ala							
	240			245		250	
gcc ccc agc cgt tgc cgc ttc ctg cgg agt gtc atg agc ctc atc gac							1060
Ala Pro Ser Arg Cys Arg Phe Leu Arg Ser Val Met Ser Leu Ile Asp							
	255			260		265	
gtg gtg gcc atc ctg ccc tac tac att ggg ctt ttg gtg ccc aag aac							1108
Val Val Ala Ile Leu Pro Tyr Tyr Ile Gly Leu Leu Val Pro Lys Asn							
	270			275		280	
gac gat gtc tct ggc gcc ttt gtc acc ctg cgt gtg ttc cgg gtg ttt							1156
Asp Asp Val Ser Gly Ala Phe Val Thr Leu Arg Val Phe Arg Val Phe							
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cgc atc ttc aag ttc tcc agg cac tca cag ggc ttg agg att ctg ggc							1204
Arg Ile Phe Lys Phe Ser Arg His Ser Gln Gly Leu Arg Ile Leu Gly							
	305			310		315	
tac aca ctc aag agc tgt gcc tct gag ctg ggc ttt ctc ctc ttt tcc							1252
Tyr Thr Leu Lys Ser Cys Ala Ser Glu Leu Gly Phe Leu Leu Phe Ser							
	320			325		330	
cta acc atg gcc atc atc atc ttt gcc act gtc atg ttt tat gct gag							1300
Leu Thr Met Ala Ile Ile Ile Phe Ala Thr Val Met Phe Tyr Ala Glu							
	335			340		345	
aag ggc aca aac aag acc aac ttt aca agc atc cct gcg gcc ttc tgg							1348
Lys Gly Thr Asn Lys Thr Asn Phe Thr Ser Ile Pro Ala Ala Phe Trp							
	350			355		360	
tat acc att gtc acc atg acc acg ctt ggc tac gga gac atg gtg ccc							1396
Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Val Pro							
	365			370		375	380



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cgc atc tac cac cag aac cag cgg gct gac aag cgc cga gca cag cag Arg Ile Tyr His Gln Asn Gln Arg Ala Asp Lys Arg Arg Ala Gln Gln 415 420 425	1540
aag gtg cgc ttg gca agg atc cga ttg gca aag agt ggt acc acc aat Lys Val Arg Leu Ala Arg Ile Arg Leu Ala Lys Ser Gly Thr Thr Asn 430 435 440	1588
gcc ttc ctg cag tac aag cag aat ggg ggc ctt gag gac agc ggc agt Ala Phe Leu Gln Tyr Lys Gln Asn Gly Gly Leu Glu Asp Ser Gly Ser 445 450 455 460	1636
ggc gag gaa cag gct ctt tgt gtc agg aac cgt tct gcc ttt gaa cag Gly Glu Glu Gln Ala Leu Cys Val Arg Asn Arg Ser Ala Phe Glu Gln 465 470 475	1684
caa cat cac cac ttg ctg cac tgt cta gag aag aca acg tgc cat gag Gln His His His Leu Leu His Cys Leu Glu Lys Thr Thr Cys His Glu 480 485 490	1732
ttc aca gat gag ctc acc ttc agt gaa gcc ctg gga gcc gtc tgc ccg Phe Thr Asp Glu Leu Thr Phe Ser Ser Glu Ala Leu Gly Ala Val Ser Pro 495 500 505	1780
ggg ggc cgc acc agc cgt agc acc tct gtg tct tcc cag cca gtg gga Gly Gly Arg Thr Ser Arg Ser Thr Ser Val Ser Ser Gln Pro Val Gly 510 515 520	1828
ccc gga agc ctg ctg tct tct tgc tgc cct cgc agg gcc aag cgc cgc Pro Gly Ser Leu Leu Ser Ser Cys Cys Pro Arg Arg Ala Lys Arg Arg 525 530 535 540	1876
gcc atc cgc ctt gcc aac tcc act gcc tca gtc agc cgt ggc agc atg Ala Ile Arg Leu Ala Asn Ser Thr Ala Ser Val Ser Arg Gly Ser Met 545 550 555	1924
cag gag ctg gac atg ctg gca ggg ctg cgc agg agc cat gcc cct cag Gln Glu Leu Asp Met Leu Ala Gly Leu Arg Arg Ser His Ala Pro Gln 560 565 570	1972
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cct gcc aac acc cca gat gag agc caa cct tcc tcc cct ggc ggc ggt Pro Ala Asn Thr Pro Asp Glu Ser Gln Pro Ser Ser Pro Gly Gly Gly 605 610 615 620	2116

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 Gly Arg Ala Gly Ser Thr Leu Arg Asn Ser Ser Leu Gly Thr Pro Cys  
 625 630 635

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 640 645

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<211> 646

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

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 Val Lys Ala Ser Arg Gly Asp Xaa Val Leu Val Val Asn Val Ser Gly  
 35 40 45  
 Arg Arg Phe Glu Thr Trp Lys Asn Thr Leu Asp Arg Tyr Pro Asp Thr  
 50 55 60  
 Leu Leu Gly Ser Ser Glu Lys Glu Phe Phe Tyr Asp Ala Asp Ser Gly  
 65 70 75 80  
 Glu Tyr Phe Phe Asp Arg Asp Pro Asp Met Phe Arg His Val Leu Asn  
 85 90 95  
 Phe Tyr Arg Thr Gly Arg Leu His Cys Pro Arg Gln Glu Cys Ile Gln  
 100 105 110  
 Ala Phe Asp Glu Glu Leu Ala Phe Tyr Gly Leu Val Pro Glu Leu Val  
 115 120 125  
 Gly Asp Cys Cys Leu Glu Glu Tyr Arg Asp Arg Lys Lys Glu Asn Ala  
 130 135 140  
 Glu Arg Leu Ala Glu Asp Glu Glu Ala Glu Gln Ala Gly Asp Gly Pro  
 145 150 155 160

Ala Leu Pro Ala Gly Ser Ser Leu Arg Gln Arg Leu Trp Arg Ala Phe  
 165 170 175  
 Glu Asn Pro His Thr Ser Thr Ala Ala Leu Val Phe Tyr Tyr Val Thr  
 180 185 190  
 Gly Phe Phe Ile Ala Val Ser Val Ile Ala Asn Val Val Glu Thr Ile  
 195 200 205  
 Pro Cys Arg Gly Ser Ala Arg Ser Ser Arg Glu Gln Pro Cys Gly  
 210 215 220  
 Glu Arg Phe Pro Gln Ala Phe Phe Cys Met Asp Thr Ala Cys Val Leu  
 225 230 235 240  
 Ile Phe Thr Gly Glu Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg  
 245 250 255  
 Cys Arg Phe Leu Arg Ser Val Met Ser Leu Ile Asp Val Val Ala Ile  
 260 265 270  
 Leu Pro Tyr Tyr Ile Gly Leu Leu Val Pro Lys Asn Asp Asp Val Ser  
 275 280 285  
 Gly Ala Phe Val Thr Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys  
 290 295 300  
 Phe Ser Arg His Ser Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys  
 305 310 315 320  
 Ser Cys Ala Ser Glu Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala  
 325 330 335  
 Ile Ile Ile Phe Ala Thr Val Met Phe Tyr Ala Glu Lys Gly Thr Asn  
 340 345 350  
 Lys Thr Asn Phe Thr Ser Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val  
 355 360 365  
 Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Val Pro Ser Thr Ile Ala  
 370 375 380  
 Gly Lys Ile Phe Gly Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile  
 385 390 395 400  
 Ala Leu Pro Val Pro Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His  
 405 410 415  
 Gln Asn Gln Arg Ala Asp Lys Arg Arg Ala Gln Gln Lys Val Arg Leu  
 420 425 430  
 Ala Arg Ile Arg Leu Ala Lys Ser Gly Thr Thr Asn Ala Phe Leu Gln  
 435 440 445  
 Tyr Lys Gln Asn Gly Gly Leu Glu Asp Ser Gly Ser Gly Glu Glu Gln  
 450 455 460  
 Ala Leu Cys Val Arg Asn Arg Ser Ala Phe Glu Gln Gln His His His  
 465 470 475 480  
 Leu Leu His Cys Leu Glu Lys Thr Thr Cys His Glu Phe Thr Asp Glu  
 485 490 495  
 Leu Thr Phe Ser Glu Ala Leu Gly Ala Val Ser Pro Gly Gly Arg Thr  
 500 505 510  
 Ser Arg Ser Thr Ser Val Ser Ser Gln Pro Val Gly Pro Gly Ser Leu  
 515 520 525  
 Leu Ser Ser Cys Cys Pro Arg Arg Ala Lys Arg Arg Ala Ile Arg Leu  
 530 535 540  
 Ala Asn Ser Thr Ala Ser Val Ser Arg Gly Ser Met Gln Glu Leu Asp  
 545 550 555 560  
 Met Leu Ala Gly Leu Arg Arg Ser His Ala Pro Gln Ser Arg Ser Ser  
 565 570 575  
 Leu Asn Ala Lys Pro His Asp Ser Leu Asp Leu Asn Cys Asp Ser Arg  
 580 585 590  
 Asp Phe Val Ala Ala Ile Ile Ser Ile Pro Thr Pro Pro Ala Asn Thr  
 595 600 605  
 Pro Asp Glu Ser Gln Pro Ser Ser Pro Gly Gly Gly Gly Arg Ala Gly  
 610 615 620  
 Ser Thr Leu Arg Asn Ser Ser Leu Gly Thr Pro Cys Leu Phe Pro Glu  
 625 630 635 640  
 Thr Val Lys Ile Ser Ser

645

<210> 11  
 <211> 1862  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> CDS  
 <222> (383)...(1157)  
 <223> K+Hnov15

&lt;400&gt; 11

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 actactgacc aaqatttcag gctgatcctc cagacctcga agttactctc cttactctcc 120  
 tgactcttaa ttacatcaca cctgtgtcga cactctctgg gaaaagactg aagaaataat 180  
 cttttcaaga agcagaaagc tctgtcatac ataggctgat acgccaccta ctgcaaaacc 240  
 gagctgacag cgcaggcgat gctgccagcg tttccattcc atcaccaggc tggggctgaa 300  
 taaaggcgtg cttgtgtggt agtgtctctt tttaaaaaat ctcaaagcca agaagaacaa 360  
 gctgaaatag catcttcaaa aa atg gag cgt aaa ata aac aga aga gaa aaa 412  
 Met Glu Arg Lys Ile Asn Arg Arg Glu Lys  
 1 5 10

gaa aag gag tat gaa ggg aaa cac aac agc ctg gaa gat act gat caa 460  
 Glu Lys Glu Tyr Glu Gly Lys His Asn Ser Leu Glu Asp Thr Asp Gln  
 15 20 25

gga aag aac tgc aaa tcc aca ctg atg acc ctc aac gtt ggt gga tat 508  
 Gly Lys Asn Cys Lys Ser Thr Leu Met Thr Leu Asn Val Gly Gly Tyr  
 30 35 40

tta tac att act caa aaa caa aca ctg acc aag tac cca gac act ttc 556  
 Leu Tyr Ile Thr Gln Lys Gln Thr Leu Thr Lys Tyr Pro Asp Thr Phe  
 45 50 55

ctt gaa ggt ata gta aat gga aaa atc ctc tgc ccg ttt gat gct gat 604  
 Leu Glu Gly Ile Val Asn Gly Lys Ile Leu Cys Pro Phe Asp Ala Asp  
 60 65 70

ggg cat tat ttc ata gac agg gat ggt ctc ctc ttc agg cat gtc cta 652  
 Gly His Tyr Phe Ile Asp Arg Asp Gly Leu Leu Phe Arg His Val Leu  
 75 80 85 90

aac ttc cta cga aat gga gaa ctt cta ttg ccc gaa ggg ttt cga gaa 700  
 Asn Phe Leu Arg Asn Gly Glu Leu Leu Leu Pro Glu Gly Phe Arg Glu  
 95 100 105

aat caa ctt ctt gca caa gaa gca gaa ttc ttt cag ctc aag gga ctg 748  
 Asn Gln Leu Leu Ala Gln Glu Ala Glu Phe Phe Gln Leu Lys Gly Leu  
 110 115 120

gca gag gaa gtg aaa tcc agg tgg gag aaa gaa cag cta aca ccc aga 796  
 Ala Glu Glu Val Lys Ser Arg Trp Glu Lys Glu Gln Leu Thr Pro Arg  
 125 130 135

gag act act ttc ttg gaa ata aca gat aac cac gat cgt tca caa gga 844  
 Glu Thr Thr Phe Leu Glu Ile Thr Asp Asn His Asp Arg Ser Gln Gly  
 140 145 150

tta aga atc ttc tgt aat gct cct gat ttc ata tca aaa ata aag tct 892  
 Leu Arg Ile Phe Cys Asn Ala Pro Asp Phe Ile Ser Lys Ile Lys Ser

155	160	165	170	
cgc att. gtt ctg gtg tdc aaa agc agg ctg gat. gga ttt cca gag gag				940
Arg Ile Val Leu Val Ser Lys Ser Arg Leu Asp Gly Phe Pro Glu Glu	175	180	185	
ttt tca ata tcg tca aat. atc atc caa ttt aaa tac ttc ata aag tct				980
Phe Ser Ile Ser Ser Asn Ile Ile Gln Phe Lys Tyr Phe Ile Lys Ser	190	195	200	
gaa aat ggc act cga ctt gta cta aag gaa gac aac acc ttt gtc tgt				1036
Glu Asn Gly Thr Arg Leu Val Leu Lys Glu Asp Asn Thr Phe Val Cys	205	210	215	
acc ttg gaa act ctt aag ttt gag gct atc atg atg gct tta aag tgt				1084
Thr Leu Glu Thr Leu Lys Phe Glu Ala Ile Met Met Ala Leu Lys Cys	220	225	230	
ggc ttt aga ctg ctg acc agc ctg gat tgt tcc aaa ggg tca att gtt				1132
Gly Phe Arg Leu Leu Thr Ser Leu Asp Cys Ser Lys Gly Ser Ile Val	235	240	245	250
cac agc gat gca ctt cat ttt atc a agtaattacc tgtgtcacga				1177
His Ser Asp Ala Leu His Phe Ile	255			
acaaaggcaa caagcatgca gccagcaagc ttcggaaaac cacagcatca aagacatccc				1237
aaataacatg cccagctagc tctgtactac agagccctgc tactaatcaa ttactgtgag				1297
ctaacgggtat gtaaattcta tctgttaaaga tgctcttccct ctgggggtgtt cctactgate				1357
agactcttcc acctaaaatg aaaacagtaa ccttctatat actgtaaaata aagactgaaa				1417
gcttttgcta tttattttgc cttaaagctgt ctttcaattc agattgtctt ggggtatttgc				1477
acaaaaagaa gcatgtacat tatctatcgt tcattttaagt aaatggtaaat aaaatattttt				1537
aaggggctat taatattttaa aatccttttc tactatggca aaaatctaca gagaaactga				1597
actggcaaaa ttaactacct ggagcaaaac agatgtgacag atctaactaa aacagagcta				1657
tagtgaaaaca aaatgagatt gtaagaagac attaaagcta ttgatttgat ttttccatag				1717
caagcaccaa aagcttatat tcacagttcc tgtgtttcat attagactta tagctgaatt				1777
ggtattttgc tgaaaaattcc tagaaaaactg cttgatgaca ataaaaagta aataaaaagca				1837
ctgtctacctt caaaaaaaaaa aaaaa				1862

<210> 12

<211> 258

<212> PRT

<213> H. sapiens

<400> 12.

Met	Glu	Arg	Lys	Ile	Asn	Arg	Arg	Glu	Lys	Glu	Lys	Glu	Tyr	Glu	Gly
1				5					10					15	
Lys	His	Asn	Ser	Leu	Glu	Asp	Thr	Asp	Gln	Gly	Lys	Asn	Cys	Lys	Ser
			20					25					30		
Thr	Leu	Met	Thr	Leu	Asn	Val	Gly	Gly	Tyr	Leu	Tyr	Ile	Thr	Gln	Lys
		35					40					45			
Gln	Thr	Leu	Thr	Lys	Tyr	Pro	Asp	Thr	Phe	Leu	Glu	Gly	Ile	Val	Asn
	50					55				60					
Gly	Lys	Ile	Leu	Cys	Pro	Phe	Asp	Ala	Asp	Gly	His	Tyr	Phe	Ile	Asp
65				70					75					80	
Arg	Asp	Gly	Leu	Leu	Phe	Arg	His	Val	Leu	Asn	Phe	Leu	Arg	Asn	Gly
			85					90					95		
Glu	Leu	Leu	Leu	Pro	Glu	Gly	Phe	Arg	Glu	Asn	Gln	Leu	Leu	Ala	Gln
			100					105				110			
Glu	Ala	Glu	Phe	Phe	Gln	Leu	Lys	Gly	Leu	Ala	Glu	Glu	Val	Lys	Ser
		115					120				125				

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Arg Trp Glu Lys Glu Gln Leu Thr Pro Arg Glu Thr Thr Phe Leu Glu
130 135 140
Ile Thr Asp Asn His Asp Arg Ser Gln Gly Leu Arg Ile Phe Cys Asn
145 150 155 160
Ala Pro Asp Phe Ile Ser Lys Ile Lys Ser Arg Ile Val Leu Val Ser
165 170 175
Lys Ser Arg Leu Asp Gly Phe Pro Glu Glu Phe Ser Ile Ser Ser Asn
180 185 190
Ile Ile Gln Phe Lys Tyr Phe Ile Lys Ser Glu Asn Gly Thr Arg Leu
195 200 205
Val Leu Lys Glu Asp Asn Thr Phe Val Cys Thr Leu Glu Thr Leu Lys
210 215 220
Phe Glu Ala Ile Met Met Ala Leu Lys Cys Gly Phe Arg Leu Leu Thr
225 230 235 240
Ser Leu Asp Cys Ser Lys Gly Ser Ile Val His Ser Asp Ala Leu His
245 250 255
Phe Ile

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<210> 13
<211> 1877
<212> DNA
<213> H. sapiens

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<220>
<221> CDS
<222> (322)...(1090)
<223> K+Hnov27

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<400> 13
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gtcgggcccc acgtgaaatc cgaggctgcg cccaagcgcg ccctgtacga gtctgtgttc 120
gggtcggggg aaatctgcgg ccccaacttc cccaaaagac tttgtatccg cccctcgagg 180
cctgtggatg cgggtgggtg ggtttccgtg aaacacgacc ccctgcctct tcttccagaa 240
gccaatgggc acagaagcac caattctccc acaatagttt cacctgctat tgtttccccc 300
acccaggaca gtcggcccaa t atg tca aga cct ctg atc act aga tcc cct 351
Met Ser Arg Pro Leu Ile Thr Arg Ser Pro
1 5 10

gca tct cca ctg awc aac caa ggc atc cct act cca gca caa ctc aca 399
Ala Ser Pro Leu Xaa Asn Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr
15 20 25

aaa tcc aat gcg cct gtc cac att gat gtg ggc ggc cac atg tac acc 447
Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Gly His Met Tyr Thr
30 35 40

agc agc ctg gcc acc ctc acc aaa tac cct gaa tcc aga atc gga aga 495
Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg
45 50 55

ott ttt gat ggt aca gag ccc att gtt ttg gac agt ctc aaa cag cac 543
Leu Phe Asp Gly Thr Glu Pro Ile Val Leu Asp Ser Leu Lys Gln His
60 65 70

tat ttc att gac aga gat gga cag atg ttc aga tat atc ttg aat ttt 591
Tyr Phe Ile Asp Arg Asp Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe
75 80 85 90

cta cga aca tcc aaa ctc ctc att cct gat gat ttc aag gac tac act 639
Leu Arg Thr Ser Lys Leu Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr

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          95      100      105
    ttg tta tat gaa gag gca aaa tat ttt cag ctt cag ccc atg ttg ttg      687
    Leu Leu Tyr Glu Glu Ala Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu
          110      115      120

    gag atg gaa aga tgg aag cag gac aga gaa act ggt cga ttt tca agg      735
    Glu Met Glu Arg Trp Lys Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg
          125      130      135

    ccc tgt gag tgc ctc gtc gtg cgt gtg gcc cca gac ctc gga gaa agg      783
    Pro Cys Glu Cys Leu Val Val Arg Val Ala Pro Asp Leu Gly Glu Arg
          140      145      150

    atc acg cta agc ggt gac aaa tcc ttg ata gaa gaa gta ttt cca gag      831
    Ile Thr Leu Ser Gly Asp Lys Ser Leu Ile Glu Glu Val Phe Pro Glu
          155      160      165      170

    atc ggc gac gtg atg tgt aac tct gtc aat gca ggc tgg aat cac gac      879
    Ile Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly Trp Asn His Asp
          175      180      185

    tcg acg cac gtc atc agg ttt cca cta aat ggc tac tgt cac ctc aac      927
    Ser Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr Cys His Leu Asn
          190      195      200

    tca gtc cag gtc ctc gag agg ttg cag caa aga gga ttt gaa atc gtg      975
    Ser Val Gln Val Leu Glu Arg Leu Gln Gln Arg Gly Phe Glu Ile Val
          205      210      215

    ggc tcc tgt ggg gga gga gta gac tcg tcc cag ttc agc gaa tac gtc      1023
    Gly Ser Cys Gly Gly Gly Val Asp Ser Ser Gln Phe Ser Glu Tyr Val
          220      225      230

    ctt cgg cgg gaa ctg agg cgg acg ccc cgt gta ccc tcc gtc atc cgg      1071
    Leu Arg Arg Glu Leu Arg Arg Thr Pro Arg Val Pro Ser Val Ile Arg
          235      240      245      250

    ata aag caa gag cct ctg g actaaatgga catatttctt atgcaaaaag      1120
    Ile Lys Gln Glu Pro Leu
          255

    gaaaacacac acaaccaata actcaaacaa aaaagggaca tttatgtgca gttgggacag      1180
    caaaccaagt cctggacgta aaattgaata aaagacacat ttatatccaa tagagaccac      1240
    acctgtattc atatgggaac aattggaata gtgatattcct caaggtgtaa aaaatatata      1300
    aatatatata tatatgtcaa aaggtaggaa atgcaaaaaa gaaaaaaaaa aaaggtgaca      1360
    gccgcagttg gtgctgtgat ggccgtgaag tgtcctgggc ctcccagaggc ctctgacaaa      1420
    taacaagcc atgagtggg aggacacagt ctcttacag ttccattgc caacaacagc      1480
    catccatatt tcttttttcc tttgtctttc ttttcccttt ttttttaaaa aaacaaaaca      1540
    aacaaaacac cttgaatcaa gtttggttgt atatggaggt tccacgtctt tctttaggca      1600
    gggaccaggc aggacttcag aaaaaccctc atgagcacat tgcaaagatg ttagacatga      1660
    aatttttaaat gtatgttgta cagaagtcac acttttttgt ccacctcaca gatgtgaact      1720
    ttactttgtt ttaaaactga tcagttttgc caaggggcca gaattattcc ttgttagaat      1780
    tgctccagtt caagtctgct gctttcctac aatttttcaa attttataat gtattaaata      1840
    caataaactc tgttttaaaa ataaaaaaaa aaaaaaa      1877

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&lt;210&gt; 14

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(256)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 14

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Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
 1           5           10           15
Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
          20           25           30
His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
          35           40           45
Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
          50           55           60
Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
          65           70           75           80
Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
          85           90           95
Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
          100          105          110
Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
          115          120          125
Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
          130          135          140
Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
          145          150          155          160
Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
          165          170          175
Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
          180          185          190
Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
          195          200          205
Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
          210          215          220
Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
          225          230          235          240
Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
          245          250          255

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&lt;210&gt; 15

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (165)...(756)

&lt;223&gt; K+Hnov2

&lt;400&gt; 15

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gcgtggtggc aggtgcctgt agccccagct acttgggagg ctgaggcagg agaatagctt      60
gaacccgggc ggcgaaggtt gagtgagccg agattgcacc actgcactcc agcctgggcg      120
acagagcgag actccatctc aaaaaaaga gtagttatgg ccac atg gcc cca cta      176
                               Met Ala Pro Leu
                               1

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tcg cca ggc gga aag gcc ttc tgc atg gtc tat gca gcc ctg ggg ctg      224
Ser Pro Gly Gly Lys Ala Phe Cys Met Val Tyr Ala Ala Leu Gly Leu
 5           10           15           20

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```

cca gcc tcc tta gct ctc gtg gcc acc ctg cgc cat tgc ctg ctg cct      272

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Pro Ala Ser Leu Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro  
 25 30 35

gtg ctc agc cgc cca cgt gcc tgg gta gcg gtc cac tgg cag ctg tca 320  
 Val Leu Ser Arg Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser  
 40 45 50

ccg gcc agg gct gcg ctg ctg cag gca gtt gca ctg gga ctg ctg gtg 368  
 Pro Ala Arg Ala Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val  
 55 60 65

gcc agc agc ttt gtg ctg ctg cca gcg ctg gtg ctg tgg ggc ctt cag 416  
 Ala Ser Ser Phe Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln  
 70 75 80

ggc gac tgc agc ctg ctg ggg gcc gtc tac ttc tgc ttc agc tgc ctc 464  
 Gly Asp Cys Ser Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu  
 85 90 95 100

agc acc att ggc ctg gag gac ttg ctg ccc ggc cgc ggc cgc agc ctg 512  
 Ser Thr Ile Gly Leu Glu Asp Leu Leu Pro Gly Arg Gly Arg Ser Leu  
 105 110 115

cac ccc gtg att tac cac ctg ggc cag ctc gca ctt ctt ggt tac ttg 560  
 His Pro Val Ile Tyr His Leu Gly Gln Leu Ala Leu Leu Gly Tyr Leu  
 120 125 130

ctt cta gga ctc ttg gcc atg ctg ctg gca gtg gag acc ttc tct gag 608  
 Leu Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu  
 135 140 145

ctg ccg cag gtc cgt gcc atg ggg aag ttc ttc aga ccc agt ggt cct 656  
 Leu Pro Gln Val Arg Ala Met Gly Lys Phe Phe Arg Pro Ser Gly Pro  
 150 155 160

gtg act gct gag gac caa ggt ggc atc cta ggg cag gat gaa ctg gct 704  
 Val Thr Ala Glu Asp Gln Gly Gly Ile Leu Gly Gln Asp Glu Leu Ala  
 165 170 175 180

ctg agc acc ctg ccg ccc gcg gcc cca gct tca gga caa gcc cct gct 752  
 Leu Ser Thr Leu Pro Pro Ala Ala Pro Ala Ser Gly Gln Ala Pro Ala  
 185 190 195

tgc t gaagcgtcag gtgaccgagt tcagctccgt aagggtggcgg cacctgagga 806  
 Cys

ggaagcagcc aggagtggct ggggaagaat ctggagatgg agccgcggtg aggggtggcgg 866  
 ggaggcctca ggggatactg ttaatcataa aaaaaaaaaa aaaaaaaaaa aaaaaaa 923

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 <211> 197  
 <212> PRT  
 <213> H. sapiens

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 20 25 30  
 Cys Leu Leu Pro Val Leu Ser Arg Pro Arg Ala Trp Val Ala Val His

35 40 45  
 Trp Gln Leu Ser Pro Ala Arg Ala Ala Leu Leu Gln Ala Val Ala Leu  
 50 55 60  
 Gly Leu Leu Val Ala Ser Ser Phe Val Leu Leu Pro Ala Leu Val Leu  
 65 70 75 80  
 Trp Gly Leu Gln Gly Asp Cys Ser Leu Leu Gly Ala Val Tyr Phe Cys  
 85 90 95  
 Phe Ser Ser Leu Ser Thr Ile Gly Leu Glu Asp Leu Leu Pro Gly Arg  
 100 105 110  
 Gly Arg Ser Leu His Pro Val Ile Tyr His Leu Gly Gln Leu Ala Leu  
 115 120 125  
 Leu Gly Tyr Leu Leu Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu  
 130 135 140  
 Thr Phe Ser Glu Leu Pro Gln Val Arg Ala Met Gly Lys Phe Phe Arg  
 145 150 155 160  
 Pro Ser Gly Pro Val Thr Ala Glu Asp Gln Gly Gly Ile Leu Gly Gln  
 165 170 175  
 Asp Glu Leu Ala Leu Ser Thr Leu Pro Pro Ala Ala Pro Ala Ser Gly  
 180 185 190  
 Gln Ala Pro Ala Cys  
 195

<210> 17  
 <211> 3102  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> CDS  
 <222> (274)...(1705)  
 <223> K+Hnov11

<400> 17

gcacgcgcaa agcgcgccacc gagaccctg ggggtggagct tgtgttaata gaaacatacc 60  
 cacccccagc ctttctctggg aggggatcag acccctcaaa ctcttgcccc agcccagccc 120  
 ttcagcacc aagaccacc aggaggcctg ggcccgccag taatgggtag ggagaggggg 180  
 ccccgccagg gcgcacggcg ctctcgccga cgetgttccc tccgcttcca ggtgtagcgc 240  
 ccccgcgcg cgcgggcggc cggcgcctcc agc atg acc ggc cag agc ctg tgg 294  
 Met Thr Gly Gln Ser Leu Trp

1

5

gac gtg tgc gag gct aac gtc gag gac ggg gag atc cgc atc aat gtg 342  
 Asp Val Ser Glu Ala Asn Val Glu Asp Gly Glu Ile Arg Ile Asn Val  
 10 15 20

ggc ggc ttc aag agg agg ctg cgc tgc cac acg ctg ctg cgc ttc ccc 390  
 Gly Gly Phe Lys Arg Arg Leu Arg Ser His Thr Leu Leu Arg Phe Pro  
 25 30 35

gag acg cgc ctg ggc cgc ttg ctg ctc tgc cac tgc cgc gag gcc att 438  
 Glu Thr Arg Leu Gly Arg Leu Leu Leu Cys His Ser Arg Glu Ala Ile  
 40 45 50 55

ctg gag ctc tgc gat gac tac gac gac gtc cag cgg gag ttc tac ttc 486  
 Leu Glu Leu Cys Asp Asp Tyr Asp Asp Val Gln Arg Glu Phe Tyr Phe  
 60 65 70

gac cgc aac cct gag ctc ttc ccc tac gtg ctg cat ttc tat cac acc 534  
 Asp Arg Asn Pro Glu Leu Phe Pro Tyr Val Leu His Phe Tyr His Thr  
 75 80 85

ggc aag ctt cac gtc atg gct gag cta tgt gtc ttc tcc ttc agc cag 582  
 Gly Lys Leu His Val Met Ala Glu Leu Cys Val Phe Ser Phe Ser Gln  
 90 95 100

gag atc gag tac tgg ggc atc aac gag ttc ttc att gac tcc tgc tgc 630  
 Glu Ile Glu Tyr Trp Gly Ile Asn Glu Phe Phe Ile Asp Ser Cys Cys  
 105 110 115

agc tac agc tac cat ggc cgc aaa gta gag ccc gag cag gag aag tgg 678  
 Ser Tyr Ser Tyr His Gly Arg Lys Val Glu Pro Glu Gln Glu Lys Trp  
 120 125 130 135

gac gag cag agt gac cag gag agc acc acg tct tcc ttc gat gag atc 726  
 Asp Glu Gln Ser Asp Gln Glu Ser Thr Thr Ser Ser Phe Asp Glu Ile  
 140 145 150

ctt gcc ttc tac aac gac gcc tcc aag ttc gat ggg cag ccc ctc ggc 774  
 Leu Ala Phe Tyr Asn Asp Ala Ser Lys Phe Asp Gly Gln Pro Leu Gly  
 155 160 165

aac ttc cgc agg cag ctg tgg ctg gcg ctg gac aac ccc ggc tac tca 822  
 Asn Phe Arg Arg Gln Leu Trp Leu Ala Leu Asp Asn Pro Gly Tyr Ser  
 170 175 180

gtg ctg agc agg gtc ttc agc atc ctg tcc atc ctg gtg gtg atg ggg 870  
 Val Leu Ser Arg Val Phe Ser Ile Leu Ser Ile Leu Val Val Met Gly  
 185 190 195

tcc atc atc acc atg tgc ctc aat agc ctg ccc gat ttc caa atc cct 918  
 Ser Ile Ile Thr Met Cys Leu Asn Ser Leu Pro Asp Phe Gln Ile Pro  
 200 205 210 215

gac agc cag ggc aac cct ggc gag gac cct agg ttc gaa atc gtg gag 966  
 Asp Ser Gln Gly Asn Pro Gly Glu Asp Pro Arg Phe Glu Ile Val Glu  
 220 225 230

cac ttt ggc att gcc tgg ttc aca ttt gag ctg gtg gcc agg ttt gct 1014  
 His Phe Gly Ile Ala Trp Phe Thr Phe Glu Leu Val Ala Arg Phe Ala  
 235 240 245

gtg gcc cct gac ttc ctc aag ttc ttc aag aat gcc cta aac ctt att 1062  
 Val Ala Pro Asp Phe Leu Lys Phe Phe Lys Asn Ala Leu Asn Leu Ile  
 250 255 260

gac ctc atg tcc atc gtc ccc ttt tac atc act ctg gtg gtg aac ctg 1110  
 Asp Leu Met Ser Ile Val Pro Phe Tyr Ile Thr Leu Val Val Asn Leu  
 265 270 275

gtg gtg gag agc aca cct act tta gcc aac ttg ggc agg gtg gcc cag 1158  
 Val Val Glu Ser Thr Pro Thr Leu Ala Asn Leu Gly Arg Val Ala Gln  
 280 285 290 295

gtc ctg agg ctg atg cgg atc ttc cgc atc tta aag ctg gcc agg cac 1206  
 Val Leu Arg Leu Met Arg Ile Phe Arg Ile Leu Lys Leu Ala Arg His  
 300 305 310

tcc act ggc ctc cgc tcc ctg ggg gcc act ttg aaa tac agc tac aaa 1254  
 Ser Thr Gly Leu Arg Ser Leu Gly Ala Thr Leu Lys Tyr Ser Tyr Lys  
 315 320 325

gaa gta ggg ctg ctc ttg ctc tac ctc tcc gtg ggg att tcc atc ttc 1302

Glu Val Gly Leu Leu Leu Leu Tyr Leu Ser Val Gly Ile Ser Ile Phe  
 330 335 340  
 tcc gtg gtg gcc tac acc att gaa aag gag gag aac gag ggc ctg gcc 1350  
 Ser Val Val Ala Tyr Thr Ile Glu Lys Glu Glu Asn Glu Gly Leu Ala  
 345 350 355  
 acc atc cct gcc tgc tgg tgg tgg gct acc gtc agt atg acc aca gtg 1398  
 Thr Ile Pro Ala Cys Trp Trp Trp Ala Thr Val Ser Met Thr Thr Val  
 360 365 370 375  
 ggg tac ggg gat gtg gtc cca ggg acc acg gca gga aag ctg act gcc 1446  
 Gly Tyr Gly Asp Val Val Pro Gly Thr Thr Ala Gly Lys Leu Thr Ala  
 380 385 390  
 tct gcc tgc atc ttg gca ggc atc ctc gtg gtg gtc ctg ccc atc acc 1494  
 Ser Ala Cys Ile Leu Ala Gly Ile Leu Val Val Val Leu Pro Ile Thr  
 395 400 405  
 ttg atc ttc aat aag ttc tcc cac ttt tac cgg cgc caa aag caa ctt 1542  
 Leu Ile Phe Asn Lys Phe Ser His Phe Tyr Arg Arg Gln Lys Gln Leu  
 410 415 420  
 gag agt gcc atg cgc agc tgt gac ttt gga gat gga atg aag gag gtc 1590  
 Glu Ser Ala Met Arg Ser Cys Asp Phe Gly Asp Gly Met Lys Glu Val  
 425 430 435  
 cct tcg gtc aat tta agg gac tat tat gcc cat aaa gtt aaa tcc ctt 1638  
 Pro Ser Val Asn Leu Arg Asp Tyr Tyr Ala His Lys Val Lys Ser Leu  
 440 445 450 455  
 atg gca agc ctg acg aac atg agc agg agc tca cca agt gaa ctc agt 1686  
 Met Ala Ser Leu Thr Asn Met Ser Arg Ser Ser Pro Ser Glu Leu Ser  
 460 465 470  
 tta aat gat tcc cta cgt t agccgggagg acttgtcacc ctccacccca 1735  
 Leu Asn Asp Ser Leu Arg  
 475  
 cattgctgag ctgcctcttg tgcctctggc acagcccagg caccttatgg ttatggtgta 1795  
 aggagtatgc ccagcccctg aggggagaga tgcattggat atgcacccag gtttctttta 1855  
 cagtttttag aatcgttttt agaggggtgg gtgtctgaca ccattgccttt gcacctttcc 1915  
 atgaaatgac actcactggt ctttgcacgt tgggcataaa atgttcacct ttttccaga 1975  
 tgagtacacc cagaatgcta atttttctgt ccattcgtgta cgctattcta gtgcttggtg 2035  
 ccagtagctg tctatgagtt gtcgtgctcc tgtttctgag gttgtcgtgt gagttctgta 2095  
 caaaaagccc ccacaagtcg tccagtagaa atgcattctat gaggtcagca aggatatgat 2155  
 gagattttgc tcacagtcac gtgaaaacaa aatctcagct ctttatccat tgctttcact 2215  
 tagttttagt accaaaacaa agagaatgca aagttaagca gacttgacca atgcaagtct 2275  
 ctaagtgtgt tttataaatg atctgtagtt ccgtggcttg catgggtgca ccaatcatct 2335  
 ttagaacgat gtacactgat gttcatctca taaatgtcac tctttagaga atgttactta 2395  
 gttaaactg cagtgaagat cgaatttttt tcccaagaac agatgtgtta gggagagggg 2455  
 cttcagctaa atagtccaaa ccctagggtg cttaaagcca agttagtga ggctgagccc 2515  
 ctgggttcac agtcaagcct ccttggttcc taggggtgact gttagagaaat gtatttcagg 2575  
 atgaggtttc tgatctaggg catttgacaa aactttgctg tgtctaatag attagcatgt 2635  
 ttttgaaata tttatttttt aagatgttta ggagtaaggc cgtgttgctc tctcaacta 2695  
 aaaagaagtt tactgttgta tcgtctccct gaggtgaacg ttgttggtgt gctagcaagg 2755  
 cagtagctta atacttttgt tgcctactct gaaagctcat caatgagagc ccttttattt 2815  
 ccaagcagaa tttagtcaga taattttgct tctaggatat agtatgttgt atatgatgct 2875  
 gtgattgccc tggagttcct gcccattgact ggaaacctgg tggatggaa gcatgtactc 2935  
 aaaatataga cgtgcacgat ggtggtgtgg cttaccacag atggaaacac tgcagttcct 2995  
 acttgcatte ccactgcctt tcatgggggg tgactgggta gaggccagga gaaaggaaag 3055

agttgtaaaa taaaaaactg ctagtgcata aaaaaaaaaa aaaaaaa

3102

&lt;210&gt; 18

&lt;211&gt; 477

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 18

Met Thr Gly Gln Ser Leu Trp Asp Val Ser Glu Ala Asn Val Glu Asp  
 1 5 10 15  
 Gly Glu Ile Arg Ile Asn Val Gly Gly Phe Lys Arg Arg Leu Arg Ser  
 20 25 30  
 His Thr Leu Leu Arg Phe Pro Glu Thr Arg Leu Gly Arg Leu Leu Leu  
 35 40 45  
 Cys His Ser Arg Glu Ala Ile Leu Glu Leu Cys Asp Asp Tyr Asp Asp  
 50 55 60  
 Val Gln Arg Glu Phe Tyr Phe Asp Arg Asn Pro Glu Leu Phe Pro Tyr  
 65 70 75 80  
 Val Leu His Phe Tyr His Thr Gly Lys Leu His Val Met Ala Glu Leu  
 85 90 95  
 Cys Val Phe Ser Phe Ser Gln Glu Ile Glu Tyr Trp Gly Ile Asn Glu  
 100 105 110  
 Phe Phe Ile Asp Ser Cys Cys Ser Tyr Ser Tyr His Gly Arg Lys Val  
 115 120 125  
 Glu Pro Glu Gln Glu Lys Trp Asp Glu Gln Ser Asp Gln Glu Ser Thr  
 130 135 140  
 Thr Ser Ser Phe Asp Glu Ile Leu Ala Phe Tyr Asn Asp Ala Ser Lys  
 145 150 155 160  
 Phe Asp Gly Gln Pro Leu Gly Asn Phe Arg Arg Gln Leu Trp Leu Ala  
 165 170 175  
 Leu Asp Asn Pro Gly Tyr Ser Val Leu Ser Arg Val Phe Ser Ile Leu  
 180 185 190  
 Ser Ile Leu Val Val Met Gly Ser Ile Ile Thr Met Cys Leu Asn Ser  
 195 200 205  
 Leu Pro Asp Phe Gln Ile Pro Asp Ser Gln Gly Asn Pro Gly Glu Asp  
 210 215 220  
 Pro Arg Phe Glu Ile Val Glu His Phe Gly Ile Ala Trp Phe Thr Phe  
 225 230 235 240  
 Glu Leu Val Ala Arg Phe Ala Val Ala Pro Asp Phe Leu Lys Phe Phe  
 245 250 255  
 Lys Asn Ala Leu Asn Leu Ile Asp Leu Met Ser Ile Val Pro Phe Tyr  
 260 265 270  
 Ile Thr Leu Val Val Asn Leu Val Val Glu Ser Thr Pro Thr Leu Ala  
 275 280 285  
 Asn Leu Gly Arg Val Ala Gln Val Leu Arg Leu Met Arg Ile Phe Arg  
 290 295 300  
 Ile Leu Lys Leu Ala Arg His Ser Thr Gly Leu Arg Ser Leu Gly Ala  
 305 310 315 320  
 Thr Leu Lys Tyr Ser Tyr Lys Glu Val Gly Leu Leu Leu Leu Tyr Leu  
 325 330 335  
 Ser Val Gly Ile Ser Ile Phe Ser Val Val Ala Tyr Thr Ile Glu Lys  
 340 345 350  
 Glu Glu Asn Glu Gly Leu Ala Thr Ile Pro Ala Cys Trp Trp Trp Ala  
 355 360 365  
 Thr Val Ser Met Thr Thr Val Gly Tyr Gly Asp Val Val Pro Gly Thr  
 370 375 380  
 Thr Ala Gly Lys Leu Thr Ala Ser Ala Cys Ile Leu Ala Gly Ile Leu  
 385 390 395 400  
 Val Val Val Leu Pro Ile Thr Leu Ile Phe Asn Lys Phe Ser His Phe  
 405 410 415  
 Tyr Arg Arg Gln Lys Gln Leu Glu Ser Ala Met Arg Ser Cys Asp Phe

420                      425                      430  
 Gly Asp Gly Met Lys Glu Val Pro Ser Val Asn Leu Arg Asp Tyr Tyr  
 435                      440                      445  
 Ala His Lys Val Lys Ser Leu Met Ala Ser Leu Thr Asn Met Ser Arg  
 450                      455                      460  
 Ser Ser Pro Ser Glu Leu Ser Leu Asn Asp Ser Leu Arg  
 465                      470                      475

&lt;210&gt; 19

&lt;211&gt; 0

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (249) ... (3495)

&lt;223&gt; K+Hnov14

&lt;400&gt; 19

gggctggttag cagggatttg tgggcggcga gggcgcgagg ggcgcgcgc catgctccgg 60  
 gccccgacgg cgcggacgcc cctcgcgcg ccagctccgg cgcgaccccg gatcccggtc 120  
 tgcgcattgc cccccgacgg ctgcgctagg agcgcggggc ccggcggggg cgcccgagct 180  
 gggcgccctc ccccggcgcg gagtccccgc accccggagg atggggcggg cagccgcggg 240  
 cgcctaag atg ccg gcc atg cgg ggc ctc ctg gcg ccg cag aac acc ttc 290  
 Met Pro Ala Met Arg Gly Leu Leu Ala Pro Gln Asn Thr Phe  
 1                      5                      10

ctg gac acc atc gct acg cgc ttc gac ggc acg cac agt aac ttc gtg 338  
 Leu Asp Thr Ile Ala Thr Arg Phe Asp Gly Thr His Ser Asn Phe Val —  
 15                      20                      25                      30

ctg ggc aac gcc agt ggc ggg gct ctt ccc gtg gtc tac tgc tct gat 386  
 Leu Gly Asn Ala Ser Gly Gly Ala Leu Pro Val Val Tyr Cys Ser Asp  
 35                      40                      45

ggc ttc tgt gac ctc acg ggc ttc tcc cgg gct gag gtc atg cag cgg 434  
 Gly Phe Cys Asp Leu Thr Gly Phe Ser Arg Ala Glu Val Met Gln Arg  
 50                      55                      60

ggc tgt gcc tgc tcc ttc ctt tat ggg cca gac acc agt gag ctc gtc 482  
 Gly Cys Ala Cys Ser Phe Leu Tyr Gly Pro Asp Thr Ser Glu Leu Val  
 65                      70                      75

cgc caa cag atc cgc aag gcc ctg gad gag cac aag gag ttc aag gct 530  
 Arg Gln Gln Ile Arg Lys Ala Leu Asp Glu His Lys Glu Phe Lys Ala  
 80                      85                      90

gag ctg atc ctg tac cgg aag agc ggg ctc ccg ttc tgg tgt ctc ctg 578  
 Glu Leu Ile Leu Tyr Arg Lys Ser Gly Leu Pro Phe Trp Cys Leu Leu  
 95                      100                      105                      110

gat gtg ata ccc ata aag aat gag aaa ggg gag gtg gct ctc ttc cta 626  
 Asp Val Ile Pro Ile Lys Asn Glu Lys Gly Glu Val Ala Leu Phe Leu  
 115                      120                      125

gtc tct cac aag gac atc agc gaa acc aag aac cga ggg ggc ccc gac 674  
 Val Ser His Lys Asp Ile Ser Glu Thr Lys Asn Arg Gly Gly Pro Asp  
 130                      135                      140

aga tgg aaa gag aca ggt ggt ggc cgg cgc cga tat ggc cgg gca cga 722  
 Arg Trp Lys Glu Thr Gly Gly Gly Arg Arg Arg Tyr Gly Arg Ala Arg

145	150	155	
tcc aaa ggc ttc aat gcc aac cgg cgg cgg agc cgg gcc gtg ctc tac			770
Ser Lys Gly Phe Asn Ala Asn Arg Arg Arg Ser Arg Ala Val Leu Tyr			
160	165	170	
cac ctg tcc ggg cac ctg cag aag cag ccc aag ggc aag cac aag ctc			818
His Leu Ser Gly His Leu Gln Lys Gln Pro Lys Gly Lys His Lys Leu			
175	180	185	190
aat aag ggg gtg ttt ggg gag aaa cca aac ttg cct gag tac aaa gta			866
Asn Lys Gly Val Phe Gly Glu Lys Pro Asn Leu Pro Glu Tyr Lys Val			
195	200	205	
gcc gcc atc cgg aag tcg ccc ttc atc ctg ttg cac tgt ggg gca ctg			914
Ala Ala Ile Arg Lys Ser Pro Phe Ile Leu Leu His Cys Gly Ala Leu			
210	215	220	
aga gcc acc tgg gat ggc ttc atc ctg ctc gcc aca ctc tat gtg gct			962
Arg Ala Thr Trp Asp Gly Phe Ile Leu Leu Ala Thr Leu Tyr Val Ala			
225	230	235	
gtc act gtg ccc tac agc gtg tgt gtg agc aca gca cgg gag ccc agt			1010
Val Thr Val Pro Tyr Ser Val Cys Val Ser Thr Ala Arg Glu Pro Ser			
240	245	250	
gcc gcc cgc ggc ccg ccc agc gtc tgt gac ctg gcc gtg gag gtc ctc			1058
Ala Ala Arg Gly Pro Pro Ser Val Cys Asp Leu Ala Val Glu Val Leu			
255	260	265	270
ttc atc ctt gac att gtg ctg aat ttc cgt acc aca ttc gtg tcc aag			1106
Phe Ile Leu Asp Ile Val Leu Asn Phe Arg Thr Thr Phe Val Ser Lys			
275	280	285	
tcg ggc cag gtg gtg ttt gcc cca aag tcc att tgc ctc cac tac gtc			1154
Ser Gly Gln Val Val Phe Ala Pro Lys Ser Ile Cys Leu His Tyr Val			
290	295	300	
acc acc tgg ttc ctg ctg gat gtc atc gca gcg ctg ccc ttt gac ctg			1202
Thr Thr Trp Phe Leu Leu Asp Val Ile Ala Ala Leu Pro Phe Asp Leu			
305	310	315	
cta cat gcc ttc aag gtc aac gtg tac ttc ggg gcc cat ctg ctg aag			1250
Leu His Ala Phe Lys Val Asn Val Tyr Phe Gly Ala His Leu Leu Lys			
320	325	330	
acg gtg cgc ctg ctg cgc ctg ctg cgc ctg ctt ccg cgg ctg gac cgg			1298
Thr Val Arg Leu Leu Arg Leu Leu Arg Leu Leu Pro Arg Leu Asp Arg			
335	340	345	350
tac tcg cag tac agc gcc gtg gtg ctg aca ctg ctc atg gcc gtg ttc			1346
Tyr Ser Gln Tyr Ser Ala Val Val Leu Thr Leu Leu Met Ala Val Phe			
355	360	365	
gcc ctg ctc gcg cac tgg gtc gcc tgc gtc tgg ttt tac att ggc cag			1394
Ala Leu Leu Ala His Trp Val Ala Cys Val Trp Phe Tyr Ile Gly Gln			
370	375	380	
cgg gag atc gag agc agc gaa tcc gag ctg cct gag att ggc tgg ctg			1442
Arg Glu Ile Glu Ser Ser Glu Ser Glu Leu Pro Glu Ile Gly Trp Leu			
385	390	395	

cag gag ctg gcc cgc cga ctg gag act ccc tac tac ctg gtg ggc cgg	1490
Gln Glu Leu Ala Arg Arg Leu Glu Thr Pro Tyr Tyr Leu Val Gly Arg	
400 405 410	
agg cca gct gga ggg aac agc tcc ggc cag agt gac aac tgc agc agc	1538
Arg Pro Ala Gly Gly Asn Ser Ser Gly Gln Ser Asp Asn Cys Ser Ser	
415 420 425 430	
agc agc gag gcc aac ggg acg ggg ctg gag ctg ctg ggc ggc ccg tcg	1586
Ser Ser Glu Ala Asn Gly Thr Gly Leu Glu Leu Leu Gly Gly Pro Ser	
435 440 445	
ctg cgc agc gcc tac atc acc tcc ctc tac ttc gca ctc agc agc ctc	1634
Leu Arg Ser Ala Tyr Ile Thr Ser Leu Tyr Phe Ala Leu Ser Ser Leu	
450 455 460	
acc agc gtg ggc ttc ggc aac gtg tcc gcc aac acg gac acc gag aag	1682
Thr Ser Val Gly Phe Gly Asn Val Ser Ala Asn Thr Asp Thr Glu Lys	
465 470 475	
atc ttc tcc atc tgc acc atg ctc atc ggc gcc ctg atg cac gcg gtg	1730
Ile Phe Ser Ile Cys Thr Met Leu Ile Gly Ala Leu Met His Ala Val	
480 485 490	
gtg ttt ggg aac gtg acg gcc atc atc cag cgc atg tac gcc cgc cgc	1778
Val Phe Gly Asn Val Thr Ala Ile Ile Gln Arg Met Tyr Ala Arg Arg	
495 500 505 510	
ttt ctg tac cac agc cgc acg cgc gac cag cgc gac tac atc cgc atc	1826
Phe Leu Tyr His Ser Arg Thr Arg Asp Gln Arg Asp Tyr Ile Arg Ile	
515 520 525	
cac cgt atc ccc aag ccc ctc aag cag cgc atg ctg gag tac ttc cag	1874
His Arg Ile Pro Lys Pro Leu Lys Gln Arg Met Leu Glu Tyr Phe Gln	
530 535 540	
gcc acc tgg gcg gtg aac aat ggc atc gac acc acc gag ctg ctg cag	1922
Ala Thr Trp Ala Val Asn Asn Gly Ile Asp Thr Thr Glu Leu Leu Gln	
545 550 555	
agc ctc cct gac gag ctg cgc gca gac atc gcc atg cac ctg cac aag	1970
Ser Leu Pro Asp Glu Leu Arg Ala Asp Ile Ala Met His Leu His Lys	
560 565 570	
gag gtc ctg cag ctg cca ctg ttt gag gcg gcc agc cgc ggc tgc ctg	2018
Glu Val Leu Gln Leu Pro Leu Phe Glu Ala Ala Ser Arg Gly Cys Leu	
575 580 585 590	
cgg gca ctg tct ctg gcc ctg cgg ccc gcc ttc tgc acg ccg ggc gag	2066
Arg Ala Leu Ser Leu Ala Leu Arg Pro Ala Phe Cys Thr Pro Gly Glu	
595 600 605	
tac ctc atc cac caa ggc gat gcc ctg cag gcc ctc tac ttt gtc tgc	2114
Tyr Leu Ile His Gln Gly Asp Ala Leu Gln Ala Leu Tyr Phe Val Cys	
610 615 620	
tct ggc tcc atg gag gtg ctc aag ggt ggc acc gtg ctc gcc atc cta	2162
Ser Gly Ser Met Glu Val Leu Lys Gly Gly Thr Val Leu Ala Ile Leu	
625 630 635	



ggg aag ggc gac ctg atc ggc tgt gag ctg ccc cgg cgg gag cag gtg Gly Lys Gly Asp Leu Ile Gly Cys Glu Leu Pro Arg Arg Glu Gln Val 640 645 650	2210
gta aag gcc aat gcc gac gtg aag ggg ctg acg tac tgc gtc ctg cag Val Lys Ala Asn Ala Asp Val Lys Gly Leu Thr Tyr Cys Val Leu Gln 655 660 665 670	2258
tgt ctg cag ctg gct ggc ctg cac gac agc ctt gcg ctg tac ccc gag Cys Leu Gln Leu Ala Gly Leu His Asp Ser Leu Ala Leu Tyr Pro Glu 675 680 685	2306
ttt gcc ccg cgc ttc agt cgt ggc ctc cga ggg gag ctc agc tac aac Phe Ala Pro Arg Phe Ser Arg Gly Leu Arg Gly Glu Leu Ser Tyr Asn 690 695 700	2354
ctg ggt got ggg gga ggc tct gca gag gtg gac acc agc tcc ctg agc Leu Gly Ala Gly Gly Gly Ser Ala Glu Val Asp Thr Ser Ser Leu Ser 705 710 715	2402
ggc gac aat acc ctt atg tcc acg ctg gag gag aag gag aca gat ggg Gly Asp Asn Thr Leu Met Ser Thr Leu Glu Glu Lys Glu Thr Asp Gly 720 725 730	2450
gag cag ggc ccc acg gtc tcc cca gcc cca gct gat gag ccc tcc agc Glu Gln Gly Pro Thr Val Ser Pro Ala Pro Ala Asp Glu Pro Ser Ser 735 740 745 750	2498
ccc ctg ctg tcc cct ggc tgc acc tcc tca tcc tca gct gcc aag ctg Pro Leu Leu Ser Pro Gly Cys Thr Ser Ser Ser Ala Ala Lys Leu 755 760 765	2546
cta tcc cca cgt cga aca gca ccc cgg cct cgt cta ggt ggc aga ggg Leu Ser Pro Arg Arg Thr Ala Pro Arg Pro Arg Leu Gly Gly Arg Gly 770 775 780	2594
agg cca ggc agg gca ggg gct ttg aag gct gag gct ggc ccc tct gct Arg Pro Gly Arg Ala Gly Ala Leu Lys Ala Glu Ala Gly Pro Ser Ala 785 790 795	2642
ccc cca cgg gcc cta gag ggg cta cgg ctg ccc ccc atg cca tgg aat Pro Pro Arg Ala Leu Glu Gly Leu Arg Leu Pro Pro Met Pro Trp Asn 800 805 810	2690
gtg ccc cca gat ctg agc ccc agg gta gta gat ggc att gaa gac ggc Val Pro Pro Asp Leu Ser Pro Arg Val Val Asp Gly Ile Glu Asp Gly 815 820 825 830	2738
tgt ggc tcg gac cag ccc aag ttc tct ttc cgc gtg ggc cag tct ggc Cys Gly Ser Asp Gln Pro Lys Phe Ser Phe Arg Val Gly Gln Ser Gly 835 840 845	2786
ccg gaa tgt agc agc agc ccc tcc cct gga cca gag agc ggc ctg ctc Pro Glu Cys Ser Ser Ser Pro Ser Pro Gly Pro Glu Ser Gly Leu Leu 850 855 860	2834
act gtt ccc cat ggg ccc agc gag gca agg aac aca gac aca ctg gac Thr Val Pro His Gly Pro Ser Glu Ala Arg Asn Thr Asp Thr Leu Asp 865 870 875	2882
aag ctt cgg cag gcg gtg aca gag ctg tca gag cag gtg ctg cag atg	2930

Lys Leu Arg Gln Ala Val Thr Glu Leu Ser Glu Gln Val Leu Gln Met  
 880 885 890  
 cgg gaa gga ctg cag tca ctt cgc cag gct gtg cag ctt gtc ctg gcg 2978  
 Arg Glu Gly Leu Gln Ser Leu Arg Gln Ala Val Gln Leu Val Leu Ala  
 895 900 905 910  
 ccc cac agg gag ggt ccg tgc cct cgg gca tcg gga gag ggg ccg tgc 3026  
 Pro His Arg Glu Gly Pro Cys Pro Arg Ala Ser Gly Glu Gly Pro Cys  
 915 920 925  
 cca gcc agc acc tcc ggg ctt ctg cag cct ctg tgt gtg gac act ggg 3074  
 Pro Ala Ser Thr Ser Gly Leu Leu Gln Pro Leu Cys Val Asp Thr Gly  
 930 935 940  
 gca tcc tcc tac tgc ctg cag ccc cca gct ggc tct gtc ttg agt ggg 3122  
 Ala Ser Ser Tyr Cys Leu Gln Pro Pro Ala Gly Ser Val Leu Ser Gly  
 945 950 955  
 act tgg ccc cac cct cgt ccg ggg cct cct ccc ctc atg gca ccc cgg 3170  
 Thr Trp Pro His Pro Arg Pro Gly Pro Pro Pro Leu Met Ala Pro Arg  
 960 965 970  
 ccc tgg ggt ccc cca gcg tct cag agc tcc ccc tgg cct cga gcc aca 3218  
 Pro Trp Gly Pro Pro Ala Ser Gln Ser Ser Pro Trp Pro Arg Ala Thr  
 975 980 985 990  
 gct ttc tgg acc tcc acc tca gac tca gag ccc cct gcc tca gga gac 3266  
 Ala Phe Trp Thr Ser Thr Ser Asp Ser Glu Pro Pro Ala Ser Gly Asp  
 995 1000 1005  
 ctc tgc tct gag ccc agc acc cct gcc tcc cct cct cct tct gag gaa 3314  
 Leu Cys Ser Glu Pro Ser Thr Pro Ala Ser Pro Pro Pro Ser Glu Glu  
 1010 1015 1020  
 ggg gct agg act ggg ccc gca gag cct gtg agc cag gct gag gct acc 3362  
 Gly Ala Arg Thr Gly Pro Ala Glu Pro Val Ser Gln Ala Glu Ala Thr  
 1025 1030 1035  
 agc act gga gag ccc cca cca ggg tca ggg ggc ctg gcc ttg ccc tgg 3410  
 Ser Thr Gly Glu Pro Pro Pro Gly Ser Gly Leu Ala Leu Pro Trp  
 1040 1045 1050  
 gac ccc cac agc ctg gag atg gtg ctt att ggc tgc cat ggc tct ggc 3458  
 Asp Pro His Ser Leu Glu Met Val Leu Ile Gly Cys His Gly Ser Gly  
 055 1060 1065 1070  
 aca gtc cag tgg acc cag gaa gaa ggc aca ggg gtc t gaggaccagc 3505  
 Thr Val Gln Trp Thr Gln Glu Glu Gly Thr Gly Val  
 1075 1080  
 cctagaactc agcgttgcca ggtgtgctgc catctgctgt tcggcccaac ctcagagtga 3565  
 aggcaggggtg gcagcctccc cacggactcc atgcggcccc ctggctcagg gcaggagacc 3625  
 tggaagcaaaa ggaggacctg gctcctgact ctcagagagg ataggctgga tccctggggc 3685  
 aggcctctcc tcggcctgct cctctgacct cccggtctcc ctctgcaggc tgggggcaga 3745  
 ggctgagga caaggaagag ctttgccatc ccctgcatgt gcccctgcct ctacctgtcc 3805  
 ccaaattttt atattaaaaa aaaaaataaa ataaactaaa aaaaaaaaaa aa 3857

&lt;210&gt; 20

&lt;211&gt; 1082

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 20

Met Pro Ala Met Arg Gly Leu Leu Ala Pro Gln Asn Thr Phe Leu Asp  
 1 5 10 15  
 Thr Ile Ala Thr Arg Phe Asp Gly Thr His Ser Asn Phe Val Leu Gly  
 20 25 30  
 Asn Ala Ser Gly Gly Ala Leu Pro Val Val Tyr Cys Ser Asp Gly Phe  
 35 40 45  
 Cys Asp Leu Thr Gly Phe Ser Arg Ala Glu Val Met Gln Arg Gly Cys  
 50 55 60  
 Ala Cys Ser Phe Leu Tyr Gly Pro Asp Thr Ser Glu Leu Val Arg Gln  
 65 70 75 80  
 Gln Ile Arg Lys Ala Leu Asp Glu His Lys Glu Phe Lys Ala Glu Leu  
 85 90 95  
 Ile Leu Tyr Arg Lys Ser Gly Leu Pro Phe Trp Cys Leu Leu Asp Val  
 100 105 110  
 Ile Pro Ile Lys Asn Glu Lys Gly Glu Val Ala Leu Phe Leu Val Ser  
 115 120 125  
 His Lys Asp Ile Ser Glu Thr Lys Asn Arg Gly Gly Pro Asp Arg Trp  
 130 135 140  
 Lys Glu Thr Gly Gly Gly Arg Arg Arg Tyr Gly Arg Ala Arg Ser Lys  
 145 150 155 160  
 Gly Phe Asn Ala Asn Arg Arg Arg Ser Arg Ala Val Leu Tyr His Leu  
 165 170 175  
 Ser Gly His Leu Gln Lys Gln Pro Lys Gly Lys His Lys Leu Asn Lys  
 180 185 190  
 Gly Val Phe Gly Glu Lys Pro Asn Leu Pro Glu Tyr Lys Val Ala Ala  
 195 200 205  
 Ile Arg Lys Ser Pro Phe Ile Leu Leu His Cys Gly Ala Leu Arg Ala  
 210 215 220  
 Thr Trp Asp Gly Phe Ile Leu Leu Ala Thr Leu Tyr Val Ala Val Thr  
 225 230 235 240  
 Val Pro Tyr Ser Val Cys Val Ser Thr Ala Arg Glu Pro Ser Ala Ala  
 245 250 255  
 Arg Gly Pro Pro Ser Val Cys Asp Leu Ala Val Glu Val Leu Phe Ile  
 260 265 270  
 Leu Asp Ile Val Leu Asn Phe Arg Thr Thr Phe Val Ser Lys Ser Gly  
 275 280 285  
 Gln Val Val Phe Ala Pro Lys Ser Ile Cys Leu His Tyr Val Thr Thr  
 290 295 300  
 Trp Phe Leu Leu Asp Val Ile Ala Ala Leu Pro Phe Asp Leu Leu His  
 305 310 315 320  
 Ala Phe Lys Val Asn Val Tyr Phe Gly Ala His Leu Leu Lys Thr Val  
 325 330 335  
 Arg Leu Leu Arg Leu Leu Arg Leu Leu Pro Arg Leu Asp Arg Tyr Ser  
 340 345 350  
 Gln Tyr Ser Ala Val Val Leu Thr Leu Leu Met Ala Val Phe Ala Leu  
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 Leu Ala His Trp Val Ala Cys Val Trp Phe Tyr Ile Gly Gln Arg Glu  
 370 375 380  
 Ile Glu Ser Ser Glu Ser Glu Leu Pro Glu Ile Gly Trp Leu Gln Glu  
 385 390 395 400  
 Leu Ala Arg Arg Leu Glu Thr Pro Tyr Tyr Leu Val Gly Arg Arg Pro  
 405 410 415  
 Ala Gly Gly Asn Ser Ser Gly Gln Ser Asp Asn Cys Ser Ser Ser Ser  
 420 425 430  
 Glu Ala Asn Gly Thr Gly Leu Glu Leu Leu Gly Gly Pro Ser Leu Arg  
 435 440 445  
 Ser Ala Tyr Ile Thr Ser Leu Tyr Phe Ala Leu Ser Ser Leu Thr Ser  
 450 455 460

Val	Gly	Phe	Gly	Asn	Val	Ser	Ala	Asn	Thr	Asp	Thr	Glu	Lys	Ile	Phe
465					470					475					480
Ser	Ile	Cys	Thr	Met	Leu	Ile	Gly	Ala	Leu	Met	His	Ala	Val	Val	Phe
				485					490					495	
Gly	Asn	Val	Thr	Ala	Ile	Ile	Gln	Arg	Met	Tyr	Ala	Arg	Arg	Phe	Leu
			500					505					510		
Tyr	His	Ser	Arg	Thr	Arg	Asp	Gln	Arg	Asp	Tyr	Ile	Arg	Ile	His	Arg
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Ile	Pro	Lys	Pro	Leu	Lys	Gln	Arg	Met	Leu	Glu	Tyr	Phe	Gln	Ala	Thr
	530					535					540				
Trp	Ala	Val	Asn	Asn	Gly	Ile	Asp	Thr	Thr	Glu	Leu	Leu	Gln	Ser	Leu
545					550					555					560
Pro	Asp	Glu	Leu	Arg	Ala	Asp	Ile	Ala	Met	His	Leu	His	Lys	Glu	Val
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Leu	Gln	Leu	Pro	Leu	Phe	Glu	Ala	Ala	Ser	Arg	Gly	Cys	Leu	Arg	Ala
			580					585					590		
Leu	Ser	Leu	Ala	Leu	Arg	Pro	Ala	Phe	Cys	Thr	Pro	Gly	Glu	Tyr	Leu
		595				600						605			
Ile	His	Gln	Gly	Asp	Ala	Leu	Gln	Ala	Leu	Tyr	Phe	Val	Cys	Ser	Gly
	610					615					620				
Ser	Met	Glu	Val	Leu	Lys	Gly	Gly	Thr	Val	Leu	Ala	Ile	Leu	Gly	Lys
625					630					635					640
Gly	Asp	Leu	Ile	Gly	Cys	Glu	Leu	Pro	Arg	Arg	Glu	Gln	Val	Val	Lys
			645						650					655	
Ala	Asn	Ala	Asp	Val	Lys	Gly	Leu	Thr	Tyr	Cys	Val	Leu	Gln	Cys	Leu
			660					665					670		
Gln	Leu	Ala	Gly	Leu	His	Asp	Ser	Leu	Ala	Leu	Tyr	Pro	Glu	Phe	Ala
		675					680					685			
Pro	Arg	Phe	Ser	Arg	Gly	Leu	Arg	Gly	Glu	Leu	Ser	Tyr	Asn	Leu	Gly
	690					695						700			
Ala	Gly	Gly	Gly	Ser	Ala	Glu	Val	Asp	Thr	Ser	Ser	Leu	Ser	Gly	Asp
705					710					715					720
Asn	Thr	Leu	Met	Ser	Thr	Leu	Glu	Glu	Lys	Glu	Thr	Asp	Gly	Glu	Gln
				725					730					735	
Gly	Pro	Thr	Val	Ser	Pro	Ala	Pro	Ala	Asp	Glu	Pro	Ser	Ser	Pro	Leu
			740					745					750		
Leu	Ser	Pro	Gly	Cys	Thr	Ser	Ser	Ser	Ser	Ala	Ala	Lys	Leu	Leu	Ser
		755					760					765			
Pro	Arg	Arg	Thr	Ala	Pro	Arg	Pro	Arg	Leu	Gly	Gly	Arg	Gly	Arg	Pro
	770					775						780			
Gly	Arg	Ala	Gly	Ala	Leu	Lys	Ala	Glu	Ala	Gly	Pro	Ser	Ala	Pro	Pro
785					790					795					800
Arg	Ala	Leu	Glu	Gly	Leu	Arg	Leu	Pro	Pro	Met	Pro	Trp	Asn	Val	Pro
				805					810					815	
Pro	Asp	Leu	Ser	Pro	Arg	Val	Val	Asp	Gly	Ile	Glu	Asp	Gly	Cys	Gly
		820						825					830		
Ser	Asp	Gln	Pro	Lys	Phe	Ser	Phe	Arg	Val	Gly	Gln	Ser	Gly	Pro	Glu
		835					840					845			
Cys	Ser	Ser	Ser	Pro	Ser	Pro	Gly	Pro	Glu	Ser	Gly	Leu	Leu	Thr	Val
	850					855					860				
Pro	His	Gly	Pro	Ser	Glu	Ala	Arg	Asn	Thr	Asp	Thr	Leu	Asp	Lys	Leu
865					870					875					880
Arg	Gln	Ala	Val	Thr	Glu	Leu	Ser	Glu	Gln	Val	Leu	Gln	Met	Arg	Glu
				885					890					895	
Gly	Leu	Gln	Ser	Leu	Arg	Gln	Ala	Val	Gln	Leu	Val	Leu	Ala	Pro	His
		900					905					910			
Arg	Glu	Gly	Pro	Cys	Pro	Arg	Ala	Ser	Gly	Glu	Gly	Pro	Cys	Pro	Ala
	915						920					925			
Ser	Thr	Ser	Gly	Leu	Leu	Gln	Pro	Leu	Cys	Val	Asp	Thr	Gly	Ala	Ser
	930					935					940				
Ser	Tyr	Cys	Leu	Gln	Pro	Ala	Gly	Ser	Val	Leu	Ser	Gly	Thr	Trp	

945					950					955					960
Pro	His	Pro	Arg	Pro	Gly	Pro	Pro	Pro	Leu	Met	Ala	Pro	Arg	Pro	Trp
				965					970					975	
Gly	Pro	Pro	Ala	Ser	Gln	Ser	Ser	Pro	Trp	Pro	Arg	Ala	Thr	Ala	Phe
			980					985					990		
Trp	Thr	Ser	Thr	Ser	Asp	Ser	Glu	Pro	Pro	Ala	Ser	Gly	Asp	Leu	Cys
		995					1000					1005			
Ser	Glu	Pro	Ser	Thr	Pro	Ala	Ser	Pro	Pro	Pro	Ser	Glu	Glu	Gly	Ala
	1010				1015						1020				
Arg	Thr	Gly	Pro	Ala	Glu	Pro	Val	Ser	Gln	Ala	Glu	Ala	Thr	Ser	Thr
1025					1030					1035					104
Gly	Glu	Pro	Pro	Pro	Gly	Ser	Gly	Gly	Leu	Ala	Leu	Pro	Trp	Asp	Pro
			1045						1050					1055	
His	Ser	Leu	Glu	Met	Val	Leu	Ile	Gly	Cys	His	Gly	Ser	Gly	Thr	Val
		1060						1065					1070		
Gln	Trp	Thr	Gln	Glu	Glu	Gly	Thr	Gly	Val						
		1075					1080.								

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<212> DNA
<213> H. sapiens
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<222> (346)...(1057)
<223> K+Hnov28, splice 1
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acatgtagaa	ggccctaggg	gaatgctttc	ttccccagat	ctttgccctg	tagtaggttt 180
cagctgagca	aggacgagta	gtttttctgg	tgtttggcct	cctctgtttg	gtggaaaaag 240
actttcttct	ctattttcct	agttatatat	gctatcatat	gtctgttttt	ctcctcttga 300
agtttccttg	aaacctgggc	tcttgaagac	gcatactctg	agcag atg gat aat gga	357
					Met Asp Asn Gly

gac tgg ggc tat atg atg act gac cca gtc aca tta aat gta ggt gga 405  
Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu Asn Val Gly Gly  
5 10 15 20

cac ttg tat aca acg tct ctc acc aca ttg acg cgt tac ccg gat tcc 453  
His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg Tyr Pro Asp Ser  
25 30 35

atg ctt gga gct atg ttt ggg ggg gac ttc ccc aca gct cga gac cct 501  
Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr Ala Arg Asp Pro  
40 45 50

caa ggc aat tac ttt att gat cga gat gga cct ctt ttc cga tat gtc 549  
Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu Phe Arg Tyr Val  
55 60 65

ctc aac ttc tta aga act tca gaa ttg acc tta ccg ttg gat ttt aag 597  
Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro Leu Asp Phe Lys  
70 75 80

gaa ttt gat ctg ctt cgg aaa gaa gca gat ttt tac cag att gag ccc 645  
Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr Gln Ile Glu Pro  
85 90 95 100

ttg att cag tgt ctc aat gat cct aag cct ttg tat ccc atg gat act 693  
 Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr Pro Met Asp Thr  
 105 110 115  
 ttt gaa gaa gtt gtg gag ctg tct agt act cgg aag ctt tct aag tac 741  
 Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys Leu Ser Lys Tyr  
 120 125 130  
 tcc aac cca gtg gct gtc atc ata acg caa cta acc atc acc act aag 789  
 Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr Ile Thr Thr Lys  
 135 140 145  
 gtc cat tcc tta cta gha ggc atc tca aat tat ttt acc aag tgg aat 837  
 Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe Thr Lys Trp Asn  
 150 155 160  
 aag cac atg atg gac acc aga gac tgc cag gtt tcc ttt act ttt gga 885  
 Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser Phe Thr Phe Gly  
 165 170 175 180  
 ccc tgt gat tat cac cag gaa gtt tct ctt agg gtc cac ctg atg gaa 933  
 Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val His Leu Met Glu  
 185 190 195  
 tac att aca aaa caa ggt ttc acg atc cgc aac acc cgg gtg cat cac 981  
 Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr Arg Val His His  
 200 205 210  
 atg agt gag cgg gcc aat gaa aac aca gtg gag cac aac tgg act ttc 1029  
 Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His Asn Trp Thr Phe  
 215 220 225  
 tgt agg cta gcc cgg aag aca gac gac t gatctccgac cctgccacag 1077  
 Cys Arg Leu Ala Arg Lys Thr Asp Asp  
 230 235  
 gttcctggaa agactctcca ggaaatggaa gatactgatt ttttttttta aatcacagtg 1137  
 tgagatattt tttttctttt aaatagttgt atttatttga aggcagtgag gaccagaagg 1197  
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 tataatctac ccttaacaga gcttttctta ttacagtgtt aaaatgattt ctgataaaat 1377  
 ggtccctaac tcaactagaa ggctaaaaat acaagaatga aagaataagc agagtactca 1437  
 tgatgccttt gagaaaaatc aaaacatcat gtaggggtgac ctagtttcca aaccaataaa 1497  
 taagtagtat tgtaatatta aaggaaaact gttccaatca tttaaaagta ctatttaagt 1557  
 actgcttttt acagttatga caactgtttc tttctatgca tataaatcaa ggaaccaaatt 1617  
 atctgtagcc atggaaaatgt ctgactagaa atatttatat tgaattctga atacaaaatg 1677  
 tccctgtggt agaaaaactta ctctttatgc ctgggtgcagt ataattccca agtggtactgt 1737  
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 aaa 1800

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 <223> K+Hnov28 splice 2

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ttgtagagaa aaatccattt ctgcagtggg atgggttaagg ataatacaca cataatcaca 180  
ttatccttgt atgcctggct acttggtgctg gctgtatgt gaatgttaac cccaaagact 240  
ccttttagatg tcgctgaact agttactata aaaagtattt cgctttcaaa ctcccacatt 300  
tcaagaagag caaaactcaa tacaaggcaa ttttgaagtt tccctgaaac ctgggctctt 360  
gaagacgcat cactggagca g atg gat aat gga gac tgg ggc tat atg atg 411  
Met Asp Asn Gly Asp Trp Gly Tyr Met Met  
1 5 10

act gac cca gtc aca tta aat gta ggt gga cac ttg tat aca acg tct 459  
Thr Asp Pro Val Thr Leu Asn Val Gly Gly His Leu Tyr Thr Thr Ser  
15 20 25

ctc acc aca ttg acg cgt tac ccg gat tcc atg ctt gga gct atg ttt 507  
Leu Thr Thr Leu Thr Arg Tyr Pro Ser Met Leu Gly Ala Met Phe  
30 35 40

ggg ggg gac ttc ccc aca gct cga gap cct caa ggc aat tac ttt att 555  
Gly Gly Asp Phe Pro Thr Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile  
45 50 55

gat cga gat gga cct ctt ttc cga tat gtc ctc aac ttc tta aga act 603  
Asp Arg Asp Gly Pro Leu Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr  
60 65 70

tca gaa ttg acc tta ccg ttg gat ttt aag gaa ttt gat ctg ctt cgg 651  
Ser Glu Leu Thr Leu Pro Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg  
75 80 85 90

aaa gaa gca gat ttt tac cag att gag ccc ttg att cag tgt ctc aat 699  
Lys Glu Ala Asp Phe Tyr Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn  
95 100 105

gat cct aag cct ttg tat ccc atg gat act ttt gaa gaa gtt gtg gag 747  
Asp Pro Lys Pro Leu Tyr Pro Met Asp Thr Phe Glu Glu Val Val Glu  
110 115 120

ctg tct agt act cgg aag ctt tct aag tac tcc aac cca gtg gct gtc 795  
Leu Ser Ser Thr Arg Lys Leu Ser Lys Tyr Ser Asn Pro Val Ala Val  
125 130 135

atc ata acg caa cta acc atc acc act aag gtc cat tcc tta cta gaa 843  
Ile Ile Thr Gln Leu Thr Ile Thr Thr Lys Val His Ser Leu Leu Glu  
140 145 150

ggc atc tca aat tat ttt acc aag tgg aat aag cac atg atg gac acc 891  
Gly Ile Ser Asn Tyr Phe Thr Lys Trp Asn Lys His Met Met Asp Thr  
155 160 165 170

aga gac tgc cag gtt tcc ttt act ttt gga ccc tgt gat tat cac cag 939  
Arg Asp Cys Gln Val Ser Phe Thr Phe Gly Pro Cys Asp Tyr His Gln  
175 180 185

gaa gtt tct ctt agg gtc cac ctg atg gaa tac att aca aaa caa ggt 987  
Glu Val Ser Leu Arg Val His Leu Met Glu Tyr Ile Thr Lys Gln Gly  
190 195 200

ttc acg atc cgc aac acc cgg gtg cat cac atg agt gag cgg gcc aat 1035  
Phe Thr Ile Arg Asn Thr Arg Val His Met Ser Glu Arg Ala Asn

205 210 215

gaa aac aca gtg gag cac aac tgg act ttc tgt agg cta gcc cgg aag 1083  
 Glu Asn Thr Val Glu His Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys  
 220 225 230

aca gac gac t gatctccgac cctgccacag gttcctggaa agactctcca 1133  
 Thr Asp Asp  
 235

ggaaatggaa gatactgatt ttttttttta aatcdacagt tgagatattt tttttctttt 1193  
 aaatagttgt atttatttga aggcagtga gaccagaagg aagttttgtg ctttggcaga 1253  
 ctccctccatg ttttgttccc ttccccctga gtatgcatgt gcctgttcag agtctccaga 1313  
 tacctttttt ataaaaagaa gtctgaaaaat cattatggta tataatctac ccttaacaga 1373  
 gctttttotta ttacagtgtt aaaatgattt ctgataaaat ggtccctaac tcaactagaa 1433  
 ggctaaaaat acaagaatga aagaataagc agagtactca tgatgccttt gagaaaaatc 1493  
 aaaacatcat gtaggggtgac ctagtttcca aaccaataaa taagtagtat tgtaatatta 1553  
 aaggaaaact gttccaatca tttaaaagta cttattaagt actgcttttt acagttatga 1613  
 caactgtttc tttctatgca tataaatcaa ggaaccaa atctgtagcc atggaaatgt 1673  
 ctgactagaa atatttatat tgaattctga atacaaaatg tccctgtggt agaaaactta 1733  
 ctctttatgc ctgggtgcagt ataattccca agtgtactgt ctaccagaaa aaaaaacaa 1793  
 aactaataaa aatgaaata tgaaaaaaa aaaaaaaaaaaa aaa 1836

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 aactgtttgt ttaaattgctt ttgaattgta gataaaaaata aattcacatt ggcatcatta 180  
 gtatctgagc atttctcagt gtcttaaggc tggctctcca tgagtgtctg ctgattgact 240  
 ctcatctata tcgtttccct gaaacctggg ctcttgaaga cgcactactg gagcag atg 299  
 Met  
 1

gat aat gga gac tgg ggc tat atg atg act gac cca gtc aca tta aat 347  
 Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu Asn  
 5 10 15

gta ggt gga cac ttg tat aca acg tct ctc acc aca ttg acg cgt tac 395  
 Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg Tyr  
 20 25 30

ccg gat tcc atg ctt gga gct atg ttt ggg ggg gac ttc ccc aca gct 443  
 Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr Ala  
 35 40 45

cga gac cct caa ggc aat tac ttt att gat cga gat gga cct ctt ttc 491  
 Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu Phe  
 50 55 60 65

cga tat gtc ctc aac ttc tta aga act tca gaa ttg acc tta ccg ttg 539  
 Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro Leu  
 70 75 80



gat ttt aag gaa ttt gat ctg ctt cgg aaa gaa gca gat ttt tac cag 587  
 Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr Gln  
 85 90 95  
 att gag ccc ttg att cag tgt ctc aat gat cct aag cct ttg tat ccc 635  
 Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr Pro  
 100 105 110  
 atg gat act ttt gaa gaa gtt gtg gag ctg tct agt act cgg aag ctt 683  
 Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys Leu  
 115 120 125  
 tct aag tac tcc aac cca gtg gct gtc atc ata acg caa cta acc atc 731  
 Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr Ile  
 130 135 140 145  
 acc act aag gtc cat tcc tta cta gaa ggc atc tca aat tat ttt acc 779  
 Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe Thr  
 150 155 160  
 aag tgg aat aag cac atg atg gac acc aga gac tgc cag gtt tcc ttt 827  
 Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser Phe  
 165 170 175  
 act ttt gga ccc tgt gat tat cac cag gaa gtt tct ctt agg gtc cac 875  
 Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val His  
 180 185 190  
 ctg atg gaa tac att aca aaa caa ggt ttc acg atc cgc aac acc cgg 923  
 Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr Arg  
 195 200 205  
 gtg cat cac atg agt gag cgg gcc aat gaa aac aca gtg gag cac aac 971  
 Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His Asn  
 210 215 220 225  
 tgg act ttc tgt agg cta gcc cgg aag aca gac gac t gatctccgac 1018  
 Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp  
 230 235  
 cctgccacag gttcctggaa agactctcca ggaaatggaa gatactgatt ttttttttta 1078  
 aatcacagtg tgagatattt tttttctttt aaatagttgt atttatttga aggcagtgag 1138  
 gaccagaagg aagttttgtg ctttggcaga ctctccatg ttttgttccc tccccctga 1198  
 gtatgcatgt gcctgttcag agtctccaga tacctttttt ataaaaagaa gtctgaaaat 1258  
 cattatggta tataatctac ccttaacaga gctttttctta ttacagtgtc aaaatgattt 1318  
 ctgataaaat ggtccctaac tcaactagaa ggctaaaaat acaagaatga aagaataagc 1378  
 agagtactca tgatgccttt gagaaaaatc aaaacatcat gtagggtgac ctagtttcca 1438  
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 ggaaccaa atctgtagcc atggaaatgt ctgactagaa atatttatat tgaattctga 1618  
 atacaaaatg tccctgtggt agaaaactta ctctttatgc ctggtgcagt ataattccca 1678  
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 aaaaaaaaaaaa aaa 1751

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&lt;211&gt; 1542

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

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 <223> K+Hnov28, splice 4

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gctcttgaag acgcatcact ggagcag atg gat aat gga gac tgg ggc tat atg      114
Met Asp Asn Gly Asp Trp Gly Tyr Met
      1      5

atg act gac cca gtc ach tta aat gta ggt gga cac ttg tat aca acg      162
Met Thr Asp Pro Val Thr Leu Asn Val Gly Gly His Leu Tyr Thr Thr
      10      15      20      25

tct ctc acc aca ttg acg tgt tac ccg gat tcc atg ctt gga gct atg      210
Ser Leu Thr Thr Leu Thr Arg Tyr Pro Asp Ser Met Leu Gly Ala Met
      30      35      40

ttt ggg ggg gac ttc ccc aca gct cga gac cct caa ggc aat tac ttt      258
Phe Gly Gly Asp Phe Pro Thr Ala Arg Asp Pro Gln Gly Asn Tyr Phe
      45      50      55

att gat cga gat gga cct ctt ttc cga tat gtc ctc aac ttc tta aga      306
Ile Asp Arg Asp Gly Pro Leu Phe Arg Tyr Val Leu Asn Phe Leu Arg
      60      65      70

act tca gaa ttg acc tta ccg ttg gat ttt aag gaa ttt gat ctg ctt      354
Thr Ser Glu Leu Thr Leu Pro Leu Asp Phe Lys Glu Phe Asp Leu Leu
      75      80      85

cgg aaa gaa gca gat ttt tac cag att gag ccc ttg att cag tgt ctc      402
Arg Lys Glu Ala Asp Phe Tyr Gln Ile Glu Pro Leu Ile Gln Cys Leu
      90      95      100      105

aat gat cct aag cct ttg tat ccc atg gat act ttt gaa gaa gtt gtg      450
Asn Asp Pro Lys Pro Leu Tyr Pro Met Asp Thr Phe Glu Glu Val Val
      110      115      120

gag ctg tct agt act cgg aag ctt tct aag tac tcc aac cca gtg gct      498
Glu Leu Ser Ser Thr Arg Lys Leu Ser Lys Tyr Ser Asn Pro Val Ala
      125      130      135

gtc atc ata acg caa cta acc atc acc act aag gtc cat tcc tta cta      546
Val Ile Ile Thr Gln Leu Thr Ile Thr Thr Lys Val His Ser Leu Leu
      140      145      150

gaa ggc atc tca aat tat ttt acc aag tgg aat aag cac atg atg gac      594
Glu Gly Ile Ser Asn Tyr Phe Thr Lys Trp Asn Lys His Met Met Asp
      155      160      165

acc aga gac tgc cag gtt tcc ttt act ttt gga ccc tgt gat tat cac      642
Thr Arg Asp Cys Gln Val Ser Phe Thr Phe Gly Pro Cys Asp Tyr His
      170      175      180      185

cag gaa gtt tct ctt agg gtc cac ctg atg gaa tac att aca aaa caa      690
Gln Glu Val Ser Leu Arg Val His Leu Met Glu Tyr Ile Thr Lys Gln
      190      195      200

ggg ttc acg atc cgc aac acc cgg gtg cat cac atg agt gag cgg gcc      738
Gly Phe Thr Ile Arg Asn Thr Arg Val His His Met Ser Glu Arg Ala
      205      210      215

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aag aca gac gac t gatctccgac cctgccacag gttcctggaa agactctcca 839  
 Lys Thr Asp Asp  
 235

ggaaatggaa gatactgatt ttttttttta aatcacagtg tgagatattt tttttctttt 899  
 aaatagttgt atttatttga aggcagtgag gaccagaagg aagttttgtg ctttggcaga 959  
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 gcttttctta ttacagtgtt aaaatgattt ctgataaaat ggtccctaac tcaactagaa 1139  
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 caactgtttc tttctatgca tataaatcaa ggaaccaa atctgtagcc atggaaatgt 1379  
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<212> PRT

<213> H. sapiens

<400> 25

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 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu  
 50 55 60  
 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro  
 65 70 75 80  
 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr  
 85 90 95  
 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr  
 100 105 110  
 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys  
 115 120 125  
 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr  
 130 135 140  
 Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe  
 145 150 155 160  
 Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser  
 165 170 175  
 Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val  
 180 185 190  
 His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr  
 195 200 205  
 Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His  
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<210> 26

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&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (182) ... (1349)

&lt;223&gt; K+Hnov42

&lt;400&gt; 26

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ggtgggagga ggaccaggtg ggaggggtggc ggctcactca ggacccagcg ggggcagcgc      180
g atg agg cgg gtg acc ctg ttc ctg aac ggc agc ccc aag aac gga aag      229
Met Arg Arg Val Thr Leu Phe Leu Asn Gly Ser Pro Lys Asn Gly Lys
  1           5           10           15

gtg gtt gct gta tat gga act tta tct gat ttg ctt tct gtg gcc agc      277
Val Val Ala Val Tyr Gly Thr Leu Ser Asp Leu Leu Ser Val Ala Ser
           20           25           30

agt aaa ctc ggc ata aaa gcc acc agt gtg tat aat ggg aaa ggt gga      325
Ser Lys Leu Gly Ile Lys Ala Thr Ser Val Tyr Asn Gly Lys Gly Gly
           35           40           45

ctg att gat gat att gct ttg atc agg gat gat gat gtt ttg ttt gtt      373
Leu Ile Asp Asp Ile Ala Leu Ile Arg Asp Asp Asp Val Leu Phe Val
           50           55           60

tgt gaa gga gag cca ttt att gat cct cag aca gat tct aag cct cct      421
Cys Glu Gly Glu Pro Phe Ile Asp Pro Gln Thr Asp Ser Lys Pro Pro
           65           70           75           80

gag gga ttg tta gga ttc cac aca gac tgg ctg aca tta aat gtt gga      469
Glu Gly Leu Leu Gly Phe His Thr Asp Trp Leu Thr Leu Asn Val Gly
           85           90           95

ggg cgg tac ttt aca act aca cgg agc act tta gtg aat aaa gaa cct      517
Gly Arg Tyr Phe Thr Thr Thr Arg Ser Thr Leu Val Asn Lys Glu Pro
           100           105           110

gac agt atg ctg gcc cac atg ttt aag gac aaa ggt gtc tgg gga aat      565
Asp Ser Met Leu Ala His Met Phe Lys Asp Lys Gly Val Trp Gly Asn
           115           120           125

aag caa gat cat aga gga gct ttc tta att gac cga agt cct gag tac      613
Lys Gln Asp His Arg Gly Ala Phe Leu Ile Asp Arg Ser Pro Glu Tyr
           130           135           140

ttc gaa ccc att ttg aac tac ttg cgt cat gga cag ctc att gta aat      661
Phe Glu Pro Ile Leu Asn Tyr Leu Arg His Gly Gln Leu Ile Val Asn
           145           150           155           160

gat ggc att aat tta ttg ggt gtg tta gaa gaa gca aga ttt ttt ggt      709
Asp Gly Ile Asn Leu Leu Gly Val Leu Glu Glu Ala Arg Phe Phe Gly
           165           170           175

att gac tca ttg att gaa cac cta gaa gtg gca ata aag aat tct caa      757
Ile Asp Ser Leu Ile Glu His Leu Glu Val Ala Ile Lys Asn Ser Gln
           180           185           190

cca ccg gag gat cat tca cca ata tcc cga aag gaa ttt gtc cga ttt      805

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Leu	Leu	Ala	Thr	Pro	Thr	Lys	Ser	Glu	Leu	Arg	Cys	Gln	Gly	Leu	Asn		
	210					215					220						
ttc	agt	ggg	gct	gat	ctt	tct	cgt	ttg	gac	ctt	cga	tac	att	aac	ttc	901	
Phe	Ser	Gly	Ala	Asp	Leu	Ser	Arg	Leu	Asp	Leu	Arg	Tyr	Ile	Asn	Phe		
225					230					235					240		
aaa	atg	gcc	aat	tta	agc	cgc	tgt	aat	ctt	gca	cat	gca	aat	ctt	tgc	949	
Lys	Met	Ala	Asn	Leu	Ser	Arg	Cys	Asn	Leu	Ala	His	Ala	Asn	Leu	Cys		
			245					250						255			
tgt	gca	aat	ctt	gaa	cga	gct	gat	ctc	tct	gga	tca	gtg	ctt	gac	tgt	997	
Cys	Ala	Asn	Leu	Glu	Arg	Ala	Asp	Leu	Ser	Gly	Ser	Val	Leu	Asp	Cys		
		260						265					270				
gcg	aat	ctc	cag	gga	gtc	aag	atg	ctc	tgt	tct	aat	gca	gaa	gga	gca	1045	
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tcc	ctg	aaa	ctg	tgt	aat	ttt	gag	gat	cct	tct	ggg	ctt	aaa	gcc	aat	1093	
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Cys	Asp	Leu	Ser	Gly	Cys	Asp	Leu	Gln	Glu	Ala	Asn	Leu	Arg	Gly	Ser		
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Ser	Gln	Ser	Val	Arg													
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&lt;210&gt; 27

&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 27

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20 25 30
Ser Lys Leu Gly Ile Lys Ala Thr Ser Val Tyr Asn Gly Lys Gly Gly
35 40 45
Leu Ile Asp Asp Ile Ala Leu Ile Arg Asp Asp Asp Val Leu Phe Val
50 55 60
Cys Glu Gly Glu Pro Phe Ile Asp Pro Gln Thr Asp Ser Lys Pro Pro
65 70 75 80
Glu Gly Leu Leu Gly Phe His Thr Asp Trp Leu Thr Leu Asn Val Gly
85 90 95
Gly Arg Tyr Phe Thr Thr Thr Arg Ser Thr Leu Val Asn Lys Glu Pro
100 105 110
Asp Ser Met Leu Ala His Met Phe Lys Asp Lys Gly Val Trp Gly Asn
115 120 125
Lys Gln Asp His Arg Gly Ala Phe Leu Ile Asp Arg Ser Pro Glu Tyr
130 135 140
Phe Glu Pro Ile Leu Asn Tyr Leu Arg His Gly Gln Leu Ile Val Asn
145 150 155 160
Asp Gly Ile Asn Leu Leu Gly Val Leu Glu Ala Arg Phe Phe Gly
165 170 175
Ile Asp Ser Leu Ile Glu His Leu Glu Val Ala Ile Lys Asn Ser Gln
180 185 190
Pro Pro Glu Asp His Ser Pro Ile Ser Arg Lys Glu Phe Val Arg Phe
195 200 205
Leu Leu Ala Thr Pro Thr Lys Ser Glu Leu Arg Cys Gln Gly Leu Asn
210 215 220
Phe Ser Gly Ala Asp Leu Ser Arg Leu Asp Leu Arg Tyr Ile Asn Phe
225 230 235 240
Lys Met Ala Asn Leu Ser Arg Cys Asn Leu Ala His Ala Asn Leu Cys
245 250 255
Cys Ala Asn Leu Glu Arg Ala Asp Leu Ser Gly Ser Val Leu Asp Cys

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260 265 270  
 Ala Asn Leu Gln Gly Val Lys Met Leu Cys Ser Asn Ala Glu Gly Ala  
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 Ser Leu Lys Leu Cys Asn Phe Glu Asp Pro Ser Gly Leu Lys Ala Asn  
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 305 310 315 320  
 Thr Gly Ile Asn Leu Arg Val Ala Thr Leu Lys Asn Ala Lys Leu Lys  
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 340 345 350  
 Cys Asp Leu Ser Gly Cys Asp Leu Gln Glu Ala Asn Leu Arg Gly Ser  
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 Asp Trp Leu Asp Cys Ala Phe Thr Cys Gly Val His Cys His Gly Gln  
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 Gly Lys Tyr Pro Cys Leu Gln Val Phe Val Asn Leu Ser His Pro Gly  
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 Gln Lys Ala Leu Leu His Tyr Asn Glu Glu Ala Val Gln Ile Asn Pro  
 80 85 90  
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Lys Cys Phe Tyr Thr Pro Lys Cys His Gln Asp Arg Asn Asp Leu Leu  
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 Pro Phe Ser Cys Phe Tyr Ser Pro Ala Ser Gln Ser Glu Asp Val Ile  
 130 135 140  
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 Leu Ile Lys Lys Tyr Asp Gln Met Ala Ile Phe His Cys Leu Phe Trp  
 145 150 155  
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 Arg Asp Glu Val Gly Gly Lys Val Pro Tyr Ile Glu Gln His Gln Phe  
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 210 215 220  
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 acccactaga tgtgcacaag aggctgccat ccagtgtctg agaggaccga gccgtg atg 299  
 Met  
 1

ctg ggg ttt gcc atg atg ggc ttc tca gtc cta atg ttc ttc ttg ctc 347  
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 5 10 15

gga aca acc att cta aag cct ttt atg ctc agc att cag aga gaa gaa 395  
 Gly Thr Thr Ile Leu Lys Pro Phe Met Leu Ser Ile Gln Arg Glu Glu  
 20 25 30



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 Ser Thr Cys Thr Ala Ile His Thr Asp Ile Met Asp Asp Trp Leu Asp  
 35 40 45  
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 Cys Ala Phe Thr Cys Gly Val His Cys His Gly Gln Gly Lys Tyr Pro  
 50 55 60 65  
 tgt ctt cag gtg ttt gtg aac ctg agc cat cca ggt cag aaa gct ctg 539  
 Cys Leu Gln Val Phe Val Asn Leu Ser His Pro Gly Gln Lys Ala Leu  
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 aca cct aag tgc cac caa gat aga aat gat ttg ctg aac agt gct ctg 635  
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 gac ata aaa gaa ttc ttc gat cac aaa aat gga act ccc ttt tca tgc 683  
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 Phe Tyr Ser Pro Ala Ser Gln Ser Glu Asp Val Ile Leu Ile Lys Lys  
 130 135 140 145  
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 165 170 175  
 ctg tcc tta ctg tgt gaa aaa tat agc act gta gtc aga gat gag gta 875  
 Leu Ser Leu Leu Cys Glu Lys Tyr Ser Thr Val Val Arg Asp Glu Val  
 180 185 190  
 ggt gga aaa gta cct tat ata gaa cag cat cag ttc aaa ctg tgc att 923  
 Gly Gly Lys Val Pro Tyr Ile Glu Gln His Gln Phe Lys Leu Cys Ile  
 195 200 205  
 atg agg agg agc aaa gga aga gca gag aaa tct t aagacggtgg 967  
 Met Arg Arg Ser Lys Gly Arg Ala Glu Lys Ser  
 210 215 220  
 ccaaattaaa gtgctggcct tcagatgtct gtgatttctg caactgagga cctaattatg 1027  
 cctgtctgca aactaataat gtaaaaggta ataattaaag tatcatatct tcatgtggga 1087  
 aaaaaaaaaa aaaaaaaaaa aaaa 1111

&lt;210&gt; 30

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;400&gt; 30

Met Leu Gly Phe Ala Met Met Gly Phe Ser Val Leu Met Phe Phe Leu  
 1 5 10 15

50

Leu Gly Thr Thr Ile Leu Lys Pro Phe Met Leu Ser Ile Gln Arg Glu  
 20 25 30  
 Glu Ser Thr Cys Thr Ala Ile His Thr Asp Ile Met Asp Asp Trp Leu  
 35 40 45  
 Asp Cys Ala Phe Thr Cys Gly Val His Cys His Gly Gln Gly Lys Tyr  
 50 55 60  
 Pro Cys Leu Gln Val Phe Val Asn Leu Ser His Pro Gly Gln Lys Ala  
 65 70 75 80  
 Leu Leu His Tyr Asn Glu Glu Ala Val Gln Ile Asn Pro Lys Cys Phe  
 85 90 95  
 Tyr Thr Pro Lys Cys His Gln Asp Arg Asn Asp Leu Leu Asn Ser Ala  
 100 105 110  
 Leu Asp Ile Lys Glu Phe Phe Asp His Lys Asn Gly Thr Pro Phe Ser  
 115 120 125  
 Cys Phe Tyr Ser Pro Ala Ser Gln Ser Glu Asp Val Ile Leu Ile Lys  
 130 135 140  
 Lys Tyr Asp Gln Met Ala Ile Phe His Cys Leu Phe Trp Pro Ser Leu  
 145 150 155 160  
 Thr Leu Leu Gly Gly Ala Leu Ile Val Gly Met Val Arg Leu Thr Gln  
 165 170 175  
 His Leu Ser Leu Leu Cys Glu Lys Tyr Ser Thr Val Val Arg Asp Glu  
 180 185 190  
 Val Gly Gly Lys Val Pro Tyr Ile Glu Gln His Gln Phe Lys Leu Cys  
 195 200 205  
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 210 215 220

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22

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20

<210> 33  
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 <212> DNA  
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<400> 33  
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22

<210> 34  
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<400> 34  
 tgcctgcaaa gtttgaacat

20

<210> 35  
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<400> 35  
tgacatcact ggatgaactt ga 22

<210> 36  
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<400> 49  
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<210> 58

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<400> 58

tggtgggctg tggtgaccat gacaactgtg ggctatgggg acatg 45

<210> 59

<211> 47

<212> DNA

<213> Artificial Sequence

<400> 59

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<211> 47

<212> DNA

<213> Artificial Sequence

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tttttattct caatagagac agaaaccacc attgggtatg gctaccg 47

<210> 61

<211> 47

<212> DNA

<213> Artificial Sequence

<400> 61

ttcctcttct ccattgagac ccagacaacc ataggctatg gtttcag 47

<210> 62

<211> 47

<212> DNA

<213> Artificial Sequence

<400> 62

ttcctgttct cggaggagac gcagacgacc atcggctatg ggttccg 47

<210> 63

<211> 47

<212> DNA

<213> Artificial Sequence

<400> 63

ttcctcttct cccttgaatc ccaaaccacc attggctatg gcttccg 47

<210> 64

<211> 47

<212> DNA

<213> Artificial Sequence

<400> 64

tttctctttt ccctggaatc ccagacaacc attggctatg gagtccg 47

<210> 65

<211> 47

<212> DNA

<213> Artificial Sequence

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47

<210> 66

<211> 47

<212> DNA

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<400> 66

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47

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<400> 67

gcgctctact tcaccttcag cagcctcacc agtgtgggct tcggcaacgt

50

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<211> 15

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<213> Artificial Sequence

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<211> 15

<212> PRT

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<211> 15

<212> PRT

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<210> 72

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<212> PRT  
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1 5 10 15

<210> 73  
<211> 15  
<212> PRT  
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<400> 73  
Phe Leu Phe Ser Leu Glu Ser Gln Thr Thr Ile Gly Tyr Gly Val  
1 5 10 15

<210> 74  
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<400> 74  
Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly Tyr  
1 5 10 15

<210> 75  
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1 5 10 15

<210> 76  
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<400> 76  
Phe Leu Phe Ser Val Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe  
1 5 10 15

<210> 77  
<211> 15  
<212> PRT  
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<400> 77  
Phe Leu Phe Ser Leu Glu Ser Gln Thr Thr Ile Gly Tyr Gly Phe  
1 5 10 15

<210> 78  
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<212> PRT  
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<400> 78  
Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly Phe  
1 5 10 15



<210> 79  
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<400> 79  
 Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly Asn  
 1 5 10 15

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<220>  
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 <222> (110)...(1285)

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 Met Arg Arg  
 1  
 ggc gcg ctt ctg gcg ggc gcc ttg gcc gcg tac gcc gcg tac ctg gtg 166  
 Gly Ala Leu Leu Ala Gly Ala Leu Ala Ala Tyr Ala Ala Tyr Leu Val  
 5 10 15  
 ctg ggc gcg ctg ttg gtg gcg cgg ctg gag ggg ccg cac gaa gcc agg 214  
 Leu Gly Ala Leu Leu Val Ala Arg Leu Glu Gly Pro His Glu Ala Arg  
 20 25 30 35  
 ctc cga gcc gag ctg gag acg ctg cgg gcg cag ctg ctt cag cgc agc 262  
 Leu Arg Ala Glu Leu Glu Thr Leu Arg Ala Gln Leu Leu Gln Arg Ser  
 40 45 50  
 ccg tgt gtg gct gcc ccc gcc ctg gac gcc ttc gtg gag cga gtg ctg 310  
 Pro Cys Val Ala Ala Pro Ala Leu Asp Ala Phe Val Glu Arg Val Leu  
 55 60 65  
 gcg gcc gga cgg ctg ggg cgg gtc gtg ctt gct aac gct tcg ggg tcc 358  
 Ala Ala Gly Arg Leu Gly Arg Val Val Leu Ala Asn Ala Ser Gly Ser  
 70 75 80  
 gcc aac gcc tcg gac ccc gcc tgg gac ttc gcc tct gct ctc ttc ttc 406  
 Ala Asn Ala Ser Asp Pro Ala Trp Asp Phe Ala Ser Ala Leu Phe Phe  
 85 90 95  
 gcc agc acg ctg atc acc acc gtg ggc tat ggg tac aca acg cca ctg 454  
 Ala Ser Thr Leu Ile Thr Thr Val Gly Tyr Gly Tyr Thr Thr Pro Leu  
 100 105 110 115  
 act gat gcg ggc aag gcc ttc tcc atc gcc ttt gcg ctc ctg ggc gtg 502  
 Thr Asp Ala Gly Lys Ala Phe Ser Ile Ala Phe Ala Leu Leu Gly Val  
 120 125 130  
 ccg acc acc atg ctg ctg ctg acc gcc tca gcc cag cgc ctg tca ctg 550  
 Pro Thr Thr Met Leu Leu Leu Thr Ala Ser Ala Gln Arg Leu Ser Leu  
 135 140 145

ctg ctg act cac gtg ccc ctg tct tgg ctg agc atg cgt tgg ggc tgg	598
Leu Leu Thr His Val Pro Leu Ser Trp Leu Ser Met Arg Trp Gly Trp	
150 155 160	
gac ccc cgg cgg gcg gcc tgc tgg cac ttg gtg gcc ctg ttg ggg gtc	646
Asp Pro Arg Arg Ala Ala Cys Trp His Leu Val Ala Leu Leu Gly Val	
165 170 175	
gta gtg acc gtc tgc ttt ctg gtg ccg gct gtg atc ttt gcc cac ctc	694
Val Val Thr Val Cys Phe Leu Val Pro Ala Val Ile Phe Ala His Leu	
180 185 190 195	
gag gag gcb tgg agc ttc ttg gat gcc ttc tac ttc tgc ttt atc tct	742
Glu Glu Ala Trp Ser Phe Leu Asp Ala Phe Tyr Phe Cys Phe Ile Ser	
200 205 210	
ctg tcc aoc atc ggc ctg ggc gac tac gtg ccc ggg gag gcc cct ggc	790
Leu Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Ala Pro Gly	
215 220 225	
cag ccc tac cgg gcc ctc tac aag gtg ctg gtc aca gtc tac ctc ttc	838
Gln Pro Tyr Arg Ala Leu Tyr Lys Val Leu Val Thr Val Tyr Leu Phe	
230 235 240	
ctg ggc ctg gtg gcc atg gtg ctg gtg ctg cag acc ttc cgc cac gtg	886
Leu Gly Leu Val Ala Met Val Leu Val Leu Gln Thr Phe Arg His Val	
245 250 255	
tcc gac ctc cac ggc ctc acg gag ctc atc ctg ctg ccc cct ccg tgc	934
Ser Asp Leu His Gly Leu Thr Glu Leu Ile Leu Leu Pro Pro Pro Cys	
260 265 270 275	
cct gcc agt ttc aat gcg gat gag gac gat cgg gtg gac atc ctg ggc	982
Pro Ala Ser Phe Asn Ala Asp Glu Asp Asp Arg Val Asp Ile Leu Gly	
280 285 290	
ccc cag ccg gag tgc cac cag caa ctc tct gcc agc tcc cac acc gac	1030
Pro Gln Pro Glu Ser His Gln Gln Leu Ser Ala Ser Ser His Thr Asp	
295 300 305	
tac gct tcc atc ccc agg tag ctg ggg cag cct ctg cca ggc ttg ggt	1078
Tyr Ala Ser Ile Pro Arg * Leu Gly Gln Pro Leu Pro Gly Leu Gly	
310 315 320	
gtg cct ggc ctg gga ctg agg ggt cca ggc gac cag agc tgg ctg tac	1126
Val Pro Gly Leu Gly Leu Arg Gly Pro Gly Asp Gln Ser Trp Leu Tyr	
325 330 335	
agg aat gtc cac gag cac agc agg tga tct tga ggc ctt gcc gtc cac	1174
Arg Asn Val His Glu His Ser Arg * Ser * Gly Leu Ala Val His	
340 345 350	
cgt ctc tcc ttt gtt tcc cag cat ctg gct ggg atg tga agg gca gca	1222
Arg Leu Ser Phe Val Ser Gln His Leu Ala Gly Met * Arg Ala Ala	
355 360 365	
ctc cct gtc ccc atg tcc cgg gct cca ctg ggc acc aac ata acc ttg	1270
Leu Pro Val Pro Met Ser Arg Ala Pro Leu Gly Thr Asn Ile Thr Leu	
370 375 380	
ttc tct gtc ctt tct ctcatcctct ttacactgtg tctctctggc tctctggcat	1325

Phe Ser Val Leu Ser  
385

tctcgctgcc	tctgtctttc	cctcttgcgtg	tctctgtttc	tcattctctt	tcattgttccg	1385
tctgtgtctc	tcaattaacc	actcgtcaac	tgtgtattct	actgggctgt	gggctcagac	1445
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cttgatttcc	tcagctgcc	aatgggaaga	atagaagaat	ttgcccctaa	acccctcctg	1565
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gaggaagga	catcgaacta	agacctgaac	tatgagaaat	aggcaggaag	aagtgtgtacc	1865
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gcccagatct	gaatggcatg	ggaggtgctg	cccttaacca	tgacaccatt	gtaagagctg	2045
tccacatttg	tatgttgtgc	cctggaatca	gcctggttga	gctcaaatcc	caacttagcc	2105
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gcctatacac	ccagcacttt	ggaaggctga	ggaaggagga	tcgcttgagg	ccaggagttt	2285
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gatcacttga	ggccaggagt	ttgaggtctg	agtgagttat	gatggcactg	ctgcactcca	2465
gcctgcggga	cagagtgaga	ccctgtctga	aagaaagaga	gaaagaaaga	aagaaagaga	2525
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<210> 81

<211> 388

<212> PRT

<213> H. sapiens

<400> 81

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			20					25					30		
Glu	Ala	Arg	Leu	Arg	Ala	Glu	Leu	Glu	Thr	Leu	Arg	Ala	Gln	Leu	Leu
			35					40					45		
Gln	Arg	Ser	Pro	Cys	Val	Ala	Ala	Pro	Ala	Leu	Asp	Ala	Phe	Val	Glu
			50					55					60		
Arg	Val	Leu	Ala	Ala	Gly	Arg	Leu	Gly	Arg	Val	Val	Leu	Ala	Asn	Ala
65					70					75				80	
Ser	Gly	Ser	Ala	Asn	Ala	Ser	Asp	Pro	Ala	Trp	Asp	Phe	Ala	Ser	Ala
				85						90				95	
Leu	Phe	Phe	Ala	Ser	Thr	Leu	Ile	Thr	Thr	Val	Gly	Tyr	Gly	Tyr	Thr
			100					105					110		
Thr	Pro	Leu	Thr	Asp	Ala	Gly	Lys	Ala	Phe	Ser	Ile	Ala	Phe	Ala	Leu
			115					120					125		
Leu	Gly	Val	Pro	Thr	Thr	Met	Leu	Leu	Leu	Thr	Ala	Ser	Ala	Gln	Arg
			130				135						140		
Leu	Ser	Leu	Leu	Leu	Thr	His	Val	Pro	Leu	Ser	Trp	Leu	Ser	Met	Arg
145					150					155				160	
Trp	Gly	Trp	Asp	Pro	Arg	Arg	Ala	Ala	Cys	Trp	His	Leu	Val	Ala	Leu
				165						170				175	
Leu	Gly	Val	Val	Val	Thr	Val	Cys	Phe	Leu	Val	Pro	Ala	Val	Ile	Phe
				180				185						190	
Ala	His	Leu	Glu	Glu	Ala	Trp	Ser	Phe	Leu	Asp	Ala	Phe	Tyr	Phe	Cys
			195				200						205		
Phe	Ile	Ser	Leu	Ser	Thr	Ile	Gly	Leu	Gly	Asp	Tyr	Val	Pro	Gly	Glu
			210				215						220		
Ala	Pro	Gly	Gln	Pro	Tyr	Arg	Ala	Leu	Tyr	Lys	Val	Leu	Val	Thr	Val
225					230					235				240	

Tyr Leu Phe Leu Gly Leu Val Ala Met Val Leu Val Leu Gln Thr Phe  
 245 250 255  
 Arg His Val Ser Asp Leu His Gly Leu Thr Glu Leu Ile Leu Leu Pro  
 260 265 270  
 Pro Pro Cys Pro Ala Ser Phe Asn Ala Asp Glu Asp Asp Arg Val Asp  
 275 280 285  
 Ile Leu Gly Pro Gln Pro Glu Ser His Gln Gln Leu Ser Ala Ser Ser  
 290 295 300  
 His Thr Asp Tyr Ala Ser Ile Pro Arg Leu Gly Gln Pro Leu Pro Gly  
 305 310 315 320  
 Leu Gly Val Pro Gly Leu Gly Leu Arg Gly Pro Gly Asp Gln Ser Trp  
 325 330 335  
 Leu Tyr Arg Asn Val His Glu His Ser Arg Ser Gly Leu Ala Val His  
 340 345 350  
 Arg Leu Ser Phe Val Ser Gln His Leu Ala Gly Met Arg Ala Ala Leu  
 355 360 365  
 Pro Val Pro Met Ser Arg Ala Pro Leu Gly Thr Asn Ile Thr Leu Phe  
 370 375 380  
 Ser Val Leu Ser  
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&lt;210&gt; 82

&lt;211&gt; 3300

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)...(1285)

&lt;400&gt; 82

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cct gac ttg ctg gat cct aaa tct gcc gct cag aac tcc aaa ccg agg 106  
 Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys Pro Arg  
 5 10 15

ctc tgc ttt tcc acg aaa ccc aca gtg ctt gct tcc cgg gtg gag agt 154  
 Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val Glu Ser  
 20 25 30 35

gac acg acc att aat gtt atg aaa tgg aag acg gtc tcc acg ata ttc 202  
 Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr Ile Phe  
 40 45 50

ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg ttc aaa gca 250  
 Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe Lys Ala  
 55 60 65

ttg gag cag cct cat gag att tca cag agg acc acc att gtg atc cag 298  
 Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val Ile Gln  
 70 75 80

aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg acg gag ctg 346  
 Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr Glu Leu  
 85 90 95

gat gaa ctc att cag caa ata gtg gca gca ata aat gca ggg att ata 394  
 Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly Ile Ile

100	105	110	115	
ccg tta gga aac acc tcc aat caa atc agt cac tgg gat ttg gga agt				442
Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu Gly Ser				
	120	125	130	
tcc ttc ttc ttt gct ggc act gtt att aca acc ata gga ttt gga aac				490
Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe Gly Asn				
	135	140	145	
atc tca cca cgc aca gaa ggc ggc aaa ata ttc tgt atc atc tat gcc				538
Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile Tyr Ala				
	150	155	160	
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cag cta ggc acc ata ttt gga aaa gga att gcc aaa gtg gaa gat acg				634
Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu Asp Thr				
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ttt att aag tgg aat gtt agt cag acc aag att cgc atc atc tca aca				682
Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile Ser Thr				
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ttt gtg gtt atc act cta aca act att gga ttt ggt gac tac gtt gca				826
Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala				
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Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val Val Trp				
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Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met				
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 Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Lys Thr  
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## INTERNATIONAL SEARCH REPORT

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## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07H 21/04; C07K 14/705; C12N 15/09, 15/63; C12Q 1/68

US CL : 636/23.1, 24.3; 435/7.2, 69.1, 320.1; 530/350

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 636/23.1, 24.3; 435/7.2, 69.1, 320.1; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	PARTISETI, M. et al. Cloning and Characterization of a Novel Human Inward Rectifying Potassium Channel Predominantly Expressed in Small Intestine. FEBS Lett. 1998, Vol. 434, pages 171-176, see entire document.	1-9

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

\* Special categories of cited documents:

\*A\* document defining the general state of the art which is not considered to be of particular relevance

\*B\* earlier document published on or after the international filing date

\*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

\*O\* document referring to an oral disclosure, use, exhibition or other means

\*P\* document published prior to the international filing date but later than the priority date claimed

\*T\*

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\*

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

\*Y\*

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

\*A\*

document member of the same patent family

Date of the actual completion of the international search

28 MAY 1999

Date of mailing of the international search report

07 JUL 1999

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
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Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)\*

## B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, JAPIO, BIOSIS, SCISEARCH, WPIDS, GENEMBL, NGENSEQ 34, EST, A-GENESEQ 32, PIR 58, SWISS-PROT 35, SPTREMBL 16.

search terms: potassium channel, K+hnov

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING.

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:2, the nucleic acid having the sequence of SEQ ID NO:1, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:2 and K+Hnov protein of SEQ ID NO:2.

Group II, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:4, the nucleic acid having the sequence of SEQ ID NO:3, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:4 and K+Hnov protein of SEQ ID NO:4.

Group III, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:6, the nucleic acid having the sequence of SEQ ID NO:5, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:6 and K+Hnov protein of SEQ ID NO:6.

Group IV, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:8, the nucleic acid having the sequence of SEQ ID NO:7, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:8 and K+Hnov protein of SEQ ID NO:8.

Group V, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:10, the nucleic acid having the sequence of SEQ ID NO:9, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:10 and K+Hnov protein of SEQ ID NO:10.

Group VI, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:12, the nucleic acid having the sequence of SEQ ID NO:11, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:12 and K+Hnov protein of SEQ ID NO:12.

Group VII, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:14, the nucleic acid having the sequence of SEQ ID NO:13, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:14 and K+Hnov protein of SEQ ID NO:14.

Group VIII, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:16, the nucleic acid having the sequence of SEQ ID NO:15, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:16 and K+Hnov protein of SEQ ID NO:16.

Group IX, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:18, the nucleic acid having the sequence of SEQ ID NO:17, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:18 and K+Hnov protein of SEQ ID NO:18.

Group X, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:20, the nucleic acid having the sequence of SEQ ID NO:19, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:20 and K+Hnov protein of SEQ ID NO:20.

Group XI, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:25, the nucleic acid having the sequence of SEQ ID NO:21-25, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:25 and K+Hnov protein of SEQ ID NO:25.

Group XII, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:27, the nucleic acid having the sequence of SEQ ID NO:26, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing

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K+Hnov protein of SEQ ID NO:27 and K+Hnov protein of SEQ ID NO:27.

Group XIII, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:30, the nucleic acid having the sequence of SEQ ID NO:28-29, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:30 and K+Hnov protein of SEQ ID NO:30.

Group XIV, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:81, the nucleic acid having the sequence of SEQ ID NO:80, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:81 and K+Hnov protein of SEQ ID NO:81.

Group XV, claim(s)1-9, drawn to nucleic acids encoding K+Hnov protein having the amino acid sequence of SEQ ID NO:83, the nucleic acid having the sequence of SEQ ID NO:82, nucleic acids hybridizing to said nucleic acids, expression cassette comprising said nucleic acids, cell comprising said expression cassette, method for producing K+Hnov protein of SEQ ID NO:83 and K+Hnov protein of SEQ ID NO:83.

Group XVI, claim(s)10, drawn to monoclonal antibody that binds to K+Hnov.

Group XVII, claim(s)11-14, drawn to non-human transgenic animal model for K+Hnov.

The inventions listed as Groups I-XVII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I is directed to nucleic acid (SEQ ID NO:1) encoding the K+Hnov protein of SEQ ID NO:2, nucleic acids hybridizing to said nucleic acid, expression cassette comprising said nucleic acid, cell comprising said cassette, method of producing the K+Hnov of SEQ ID NO:2 and the protein of SEQ ID NO:2. The special technical feature is the disclosed nucleic acid of SEQ ID NO:1 encoding the K+Hnov protein of SEQ ID NO:2. The nucleic acids, proteins, antibody and transgenic animal model of Groups II-XVII do not share the special technical feature of Group I wherein the products of said Groups are structurally and functionally different. As shown in Table 1, pages 8-9, the H+Nov proteins of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 25, 27, 30, 81 and 83 are all structurally and functionally different, the nucleic acids encoding said proteins having different chromosome positions.

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International application No.  
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## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-9, SEQ ID NO:1 and 2

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.